

REMARKS

The specification has been amended to include a reference to SEQ ID NOS. and to include reference to the Sequence Listing being submitted on compact discs. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, Applicant petitions for any required relief including extensions of time and authorizes the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to Deposit Account No. 03-1952 referencing docket no. 529452000120.

Respectfully submitted,

Dated: July 22, 2002

By: 

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Please add the following paragraph on page 1 before the "Field of the Invention" section:

The Sequence Listing (containing SEQ ID NOS:1-360) is submitted in accordance with 37 CFR §§ 1.821-1.825 and §§1.52(e) and 1.96(c) on three compact discs labeled "Computer Readable Form (CRF)", "Copy 1" and "Copy 2", the contents of which are the same and are expressly incorporated herein by reference. The file names are A71249.ST25, contain 16,870,127 bytes, and were recorded on May 29, 2002.

Please replace the paragraph on page 9, starting at line 32 with the following:

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (SEQ ID NO:7) (W=tryptophan, S=serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Please replace the paragraph on page 11 starting at line 21 with the following:

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid (SEQ ID NO:1613) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Please amend the specification by replacing pages 52-196 with the following:
example as a result of homologous recombination with an appropriate gene targeting
vector, will result in the absence of the CA protein. When desired, tissue-specific
expression or knockout of the CA protein may be necessary.

It is also possible that the CA protein is overexpressed in carcinoma. As such,
transgenic animals can be generated that overexpress the CA protein. Depending on
the desired expression level, promoters of various strengths can be employed to
express the transgene. Also, the number of copies of the integrated transgene can be
determined and compared for a determination of the expression level of the transgene.
Animals generated by such methods find use as animal models of CA and are
additionally useful in screening for bioactive molecules to treat carcinoma.

Paragraph beginning at line 13 of page 52 has been amended as follows:

The CA nucleic acid sequences of the invention are depicted in Tables 1-112. The
sequences in Tables 1 (SEQ ID NOS:1-460) and 2 (SEQ ID NOS:461-952) depict
mouse tags, i.e. the genomic insertion sites. The sequences in Tables 3-402 3-112
include genomic sequence, mRNA and coding sequences for both mouse and human.
N/A indicates a gene that has been identified, but for which there has not been a name
ascribed. The different sequences of Tables 3-112 are assigned the following SEQ ID
Nos:

Table 3 beginning at line 20 of page 52 has been amended as follows:

Table 3 (mouse gene: Fscn1; human gene SNL)

Mouse genomic sequence (SEQ ID NO:4 953)

Mouse mRNA sequence (SEQ ID NO:2 954)

Mouse coding sequence (SEQ ID NO:3 955)

Human genomic sequence (SEQ ID NO:4 956)

Human mRNA sequence (SEQ ID NO:5 957)

Human coding sequence (SEQ ID NO:6 958)

Table 4 beginning at line 27 of page 52 has been amended as follows:

Table 4 (mouse gene Map3k6; human gene MAP3K6)

Mouse genomic sequence (SEQ ID NO:7 959)

Mouse mRNA sequence (SEQ ID NO:8 960)

Mouse coding sequence (SEQ ID NO:9 961)

Human genomic sequence (SEQ ID NO:40 962)

Human mRNA sequence (SEQ ID NO:41 963)

Human coding sequence (SEQ ID NO:42 964)

Table 5 beginning at line 36 of page 52 has been amended as follows:

Table 5 (mouse gene Fosb; human gene FOSB)

Mouse genomic sequence (SEQ ID NO:43 965)

Mouse mRNA sequence (SEQ ID NO:44 966)

Mouse coding sequence (SEQ ID NO:45 967)

Human genomic sequence (SEQ ID NO:46 968)

Human mRNA sequence (SEQ ID NO:47 969)

Human coding sequence (SEQ ID NO:48 970)

Table 6 beginning at line 5 of page 53 has been amended as follows:

Table 6 (mouse gene cmkbr7; human gene: CCR7)

Mouse genomic sequence (SEQ ID NO:49 971)

Mouse mRNA sequence (SEQ ID NO:20 972)

Mouse coding sequence (SEQ ID NO:24 973)

Human genomic sequence (SEQ ID NO:22 974)

Human mRNA sequence (SEQ ID NO:23 975)

Human coding sequence (SEQ ID NO:24 976)

Table 7 beginning at line 13 of page 53 has been amended as follows:

Table 7 (mouse gene: Ccnd1; human gene: CCND1)

Mouse genomic sequence (SEQ ID NO:25 977)

Mouse mRNA sequence (SEQ ID NO:26 978)

Mouse coding sequence (SEQ ID NO:27 979)

Human genomic sequence (SEQ ID NO:28 980)

Human mRNA sequence (SEQ ID NO:29 981)

Human coding sequence (SEQ ID NO:30 982)

Table 8 beginning at line 21 of page 53 has been amended as follows:

Table 8 (mouse gene: Ccnd3; human gene: CCND3)

Mouse genomic sequence (SEQ ID NO:34 983)

Mouse mRNA sequence (SEQ ID NO:32 984)

Mouse coding sequence (SEQ ID NO:33 985)

Human genomic sequence (SEQ ID NO:34 986)

Human mRNA sequence (SEQ ID NO:35 987)

Human coding sequence (SEQ ID NO:36 988)

Table 9 beginning at line 29 of page 53 has been amended as follows:

Table 9 (mouse gene: Wnt3; human gene: WNT3)

Mouse genomic sequence (SEQ ID NO:37 989)

Mouse mRNA sequence (SEQ ID NO:38 990)

Mouse coding sequence (SEQ ID NO:39 991)

Human genomic sequence (SEQ ID NO:40 992)

Human mRNA sequence (SEQ ID NO:41 993)

Human coding sequence (SEQ ID NO:42 994)

Table 10 beginning at line 37 of page 53 has been amended as follows:

Table 10 (mouse gene: Batf; human gene: BATF)

Mouse genomic sequence (SEQ ID NO:43 995)

Mouse mRNA sequence (SEQ ID NO:44 996)

Mouse coding sequence (SEQ ID NO:45 997)

Human genomic sequence (SEQ ID NO:46 998)

Human mRNA sequence (SEQ ID NO:47 999)

Human coding sequence (SEQ ID NO:48 1000)

Table 11 beginning at line 6 of page 54 has been amended as follows:

Table 11 (mouse gene: Irf4; human gene: IRF4)

Mouse genomic sequence (SEQ ID NO:49 1001)

Mouse mRNA sequence (SEQ ID NO:50 1002)

Mouse coding sequence (SEQ ID NO:54 1003)

Human genomic sequence (SEQ ID NO:52 1004)

Human mRNA sequence (SEQ ID NO:53 1005)

Human coding sequence (SEQ ID NO:54 1006)

Table 12 beginning at line 14 of page 54 has been amended as follows:

Table 12 (mouse gene: Notch1; human gene: NOTCH1)

Mouse genomic sequence (SEQ ID NO:55 1007)

Mouse mRNA sequence (SEQ ID NO:56 1008)

Mouse coding sequence (SEQ ID NO:57 1009)

Human genomic sequence (SEQ ID NO:58 1010)

Human mRNA sequence (SEQ ID NO:59 1011)

Human coding sequence (SEQ ID NO:60 1012)

Table 13 beginning at line 22 of page 54 has been amended as follows:

Table 13 (mouse gene: Myc; human gene MYC)

Mouse genomic sequence (SEQ ID NO:61 1013)

Mouse mRNA sequence (SEQ ID NO:62 1014)

Mouse coding sequence (SEQ ID NO:63 1015)

Human genomic sequence (SEQ ID NO:64 1016)

Human mRNA sequence (SEQ ID NO:65 1017)

Human coding sequence (SEQ ID NO:66 1018)

Table 14 beginning at line 30 of page 54 has been amended as follows:

Table 14 (mouse gene Bach2; human gene BACH2)

Mouse genomic sequence (SEQ ID NO:67 1019)

Mouse mRNA sequence (SEQ ID NO:68 1020)

Mouse coding sequence (SEQ ID NO:~~69~~ 1021)
Human genomic sequence (SEQ ID NO:~~70~~ 1022)
Human mRNA sequence (SEQ ID NO:~~71~~ 1023)
Human coding sequence (SEQ ID NO:~~72~~ 1024)

Table 15 beginning at line 38 of page 54 has been amended as follows:

Table 15 (mouse gene Wnt1; human gene WNT1)
Mouse genomic sequence (SEQ ID NO:~~73~~ 1025)
Mouse mRNA sequence (SEQ ID NO:~~74~~ 1026)
Mouse coding sequence (SEQ ID NO:~~75~~ 1027)
Human genomic sequence (SEQ ID NO:~~76~~ 1028)
Human mRNA sequence (SEQ ID NO:~~77~~ 1029)
Human coding sequence (SEQ ID NO:~~78~~ 1030)

Table 16 beginning at line 7 of page 55 has been amended as follows:

Table 16 (mouse gene Rasgrp1; human gene: RASGRP1)
Mouse genomic sequence (SEQ ID NO:~~79~~ 1031)
Mouse mRNA sequence (SEQ ID NO:~~80~~ 1032)
Mouse coding sequence (SEQ ID NO:~~81~~ 1033)
Human genomic sequence (SEQ ID NO:~~82~~ 1034)
Human mRNA sequence (SEQ ID NO:~~83~~ 1035)
Human coding sequence (SEQ ID NO:~~84~~ 1036)

Table 17 beginning at line 15 of page 55 has been amended as follows:

Table 17 (mouse gene: Nmyc1; human gene: MYCN)
Mouse genomic sequence (SEQ ID NO:~~85~~ 1037)
Mouse mRNA sequence (SEQ ID NO:~~86~~ 1038)
Mouse coding sequence (SEQ ID NO:~~87~~ 1039)
Human genomic sequence (SEQ ID NO:~~88~~ 1040)
Human mRNA sequence (SEQ ID NO:~~89~~ 1041)
Human coding sequence (SEQ ID NO:~~90~~ 1042)

Table 18 beginning at line 23 of page 55 has been amended as follows:

Table 18 (mouse gene: Myb; human gene: MYB)

Mouse genomic sequence (SEQ ID NO:91 1043)

Mouse mRNA sequence (SEQ ID NO:92 1044)

Mouse coding sequence (SEQ ID NO:93 1045)

Human genomic sequence (SEQ ID NO:94 1046)

Human mRNA sequence (SEQ ID NO:95 1047)

Human coding sequence (SEQ ID NO:96 1048)

Table 19 beginning at line 31 of page 55 has been amended as follows:

Table 19 (mouse gene: Sox4; human gene: SOX4)

Mouse genomic sequence (SEQ ID NO:97 1049)

Mouse mRNA sequence (SEQ ID NO:98 1050)

Mouse coding sequence (SEQ ID NO:99 1051)

Human genomic sequence (SEQ ID NO:100 1052)

Human mRNA sequence (SEQ ID NO:101 1053)

Human coding sequence (SEQ ID NO:102 1054)

Table 20 beginning at line 39 of page 55 has been amended as follows:

Table 20 (mouse gene: Tcof1; human gene: TCOF1)

Mouse genomic sequence (SEQ ID NO:103 1055)

Mouse mRNA sequence (SEQ ID NO:104 1056)

Mouse coding sequence (SEQ ID NO:105 1057)

Human genomic sequence (SEQ ID NO:106 1058)

Human mRNA sequence (SEQ ID NO:107 1059)

Human coding sequence (SEQ ID NO:108 1060)

Table 21 beginning at line 7 of page 56 has been amended as follows:

Table 21 (mouse gene: Pim1; human gene: PIM1)

Mouse genomic sequence (SEQ ID NO:109 1061)

Mouse mRNA sequence (SEQ ID NO:~~440~~ 1062)
Mouse coding sequence (SEQ ID NO:~~441~~ 1063)
Human genomic sequence (SEQ ID NO:~~442~~ 1064)
Human mRNA sequence (SEQ ID NO:~~443~~ 1065)
Human coding sequence (SEQ ID NO:~~444~~ 1066)

Table 22 beginning at line 16 of page 56 has been amended as follows:

Table 22 (mouse gene: Wnt3a; human gene: WNT3A)

Mouse genomic sequence (SEQ ID NO:~~445~~ 1067)
Mouse mRNA sequence (SEQ ID NO:~~446~~ 1068)
Mouse coding sequence (SEQ ID NO:~~447~~ 1069)
Human genomic sequence (SEQ ID NO:~~448~~ 1070)
Human mRNA sequence (SEQ ID NO:~~449~~ 1071)
Human coding sequence (SEQ ID NO:~~420~~ 1072)

Table 23 beginning at line 24 of page 56 has been amended as follows:

Table 23 (mouse gene: Ly6e; human gene LY6E)

Mouse genomic sequence (SEQ ID NO:~~421~~ 1073)
Mouse mRNA sequence (SEQ ID NO:~~422~~ 1074)
Mouse coding sequence (SEQ ID NO:~~423~~ 1075)
Human genomic sequence (SEQ ID NO:~~424~~ 1076)
Human mRNA sequence (SEQ ID NO:~~425~~ 1077)
Human coding sequence (SEQ ID NO:~~426~~ 1078)

Table 24 beginning at line 32 of page 56 has been amended as follows:

Table 24 (mouse gene: Rasa2; human gene RASA2)

Mouse genomic sequence (SEQ ID NO:~~427~~ 1079)
Mouse mRNA sequence (SEQ ID NO:~~428~~ 1080)
Mouse coding sequence (SEQ ID NO:~~429~~ 1081)
Human genomic sequence (SEQ ID NO:~~430~~ 1082)
Human mRNA sequence (SEQ ID NO:~~431~~ 1083)

Human coding sequence (SEQ ID NO:~~432~~ 1084)

Table 25 beginning at line 1 of page 57 has been amended as follows:

Table 25 (mouse gene: Gata1; human gene GATA1)

Mouse genomic sequence (SEQ ID NO:~~433~~ 1085)

Mouse mRNA sequence (SEQ ID NO:~~434~~ 1086)

Mouse coding sequence (SEQ ID NO:~~435~~ 1087)

Human genomic sequence (SEQ ID NO:~~436~~ 1088)

Human mRNA sequence (SEQ ID NO:~~437~~ 1089)

Human coding sequence (SEQ ID NO:~~438~~ 1090)

Table 26 beginning at line 9 of page 57 has been amended as follows:

Table 26 (mouse gene: Fkbp5; human gene FKBP5)

Mouse genomic sequence (SEQ ID NO:~~439~~ 1091)

Mouse mRNA sequence (SEQ ID NO:~~440~~ 1092)

Mouse coding sequence (SEQ ID NO:~~441~~ 1093)

Human genomic sequence (SEQ ID NO:~~442~~ 1094)

Human mRNA sequence (SEQ ID NO:~~443~~ 1095)

Human coding sequence (SEQ ID NO:~~444~~ 1096)

Table 27 beginning at line 17 of page 57 has been amended as follows:

Table 27 (mouse gene: Rel; human gene REL)

Mouse genomic sequence (SEQ ID NO:~~445~~ 1097)

Mouse mRNA sequence (SEQ ID NO:~~446~~ 1098)

Mouse coding sequence (SEQ ID NO:~~447~~ 1099)

Human genomic sequence (SEQ ID NO:~~448~~ 1100)

Human mRNA sequence (SEQ ID NO:~~449~~ 1101)

Human coding sequence (SEQ ID NO:~~450~~ 1102)

Table 28 beginning at line 25 of page 57 has been amended as follows:

Table 28 (mouse gene: Icsbp; human gene ICSBP1)

Mouse genomic sequence (SEQ ID NO:~~451~~ 1103)

Mouse mRNA sequence (SEQ ID NO:~~452~~ 1104)

Mouse coding sequence (SEQ ID NO:~~453~~ 1105)

Human genomic sequence (SEQ ID NO:~~454~~ 1106)

Human mRNA sequence (SEQ ID NO:~~455~~ 1107)

Human coding sequence (SEQ ID NO:~~456~~ 1108)

Table 29 beginning at line 33 of page 57 has been amended as follows:

Table 29 (mouse gene: Bmi1; human gene BMI1)

Mouse genomic sequence (SEQ ID NO:~~457~~ 1109)

Mouse mRNA sequence (SEQ ID NO:~~458~~ 1110)

Mouse coding sequence (SEQ ID NO:~~459~~ 1111)

Human genomic sequence (SEQ ID NO:~~460~~ 1112)

Human mRNA sequence (SEQ ID NO:~~461~~ 1113)

Human coding sequence (SEQ ID NO:~~462~~ 1114)

Table 30 beginning at line 1 of page 58 has been amended as follows:

Table 30 (mouse gene: Runx1; human gene RUNX1)

Mouse genomic sequence (SEQ ID NO:~~463~~ 1115)

Mouse mRNA sequence (SEQ ID NO:~~464~~ 1116)

Mouse coding sequence (SEQ ID NO:~~465~~ 1117)

Human genomic sequence (SEQ ID NO:~~466~~ 1118)

Human mRNA sequence (SEQ ID NO:~~467~~ 1119)

Human coding sequence (SEQ ID NO:~~468~~ 1120)

Table 31 beginning at line 10 of page 58 has been amended as follows:

Table 31 (mouse gene: Il2ra; human gene IL2RA)

Mouse genomic sequence (SEQ ID NO:~~469~~ 1121)

Mouse mRNA sequence (SEQ ID NO:~~470~~ 1122)

Mouse coding sequence (SEQ ID NO:~~471~~ 1123)

Human genomic sequence (SEQ ID NO:~~472~~ 1124)

Human mRNA sequence (SEQ ID NO:~~473~~ 1125)

Human coding sequence (SEQ ID NO:~~474~~ 1126)

Table 32 beginning at line 18 of page 58 has been amended as follows:

Table 32 (mouse gene: Nfkb1; human gene NFKB1)

Mouse genomic sequence (SEQ ID NO:~~475~~ 1127)

Mouse mRNA sequence (SEQ ID NO:~~476~~ 1128)

Mouse coding sequence (SEQ ID NO:~~477~~ 1129)

Human genomic sequence (SEQ ID NO:~~478~~ 1130)

Human mRNA sequence (SEQ ID NO:~~479~~ 1131)

Human coding sequence (SEQ ID NO:~~480~~ 1132)

Table 33 beginning at line 26 of page 58 has been amended as follows:

Table 33 (mouse gene: Fyn; human gene FYN)

Mouse genomic sequence (SEQ ID NO:~~481~~ 1133)

Mouse mRNA sequence (SEQ ID NO:~~482~~ 1134)

Mouse coding sequence (SEQ ID NO:~~483~~ 1135)

Human genomic sequence (SEQ ID NO:~~484~~ 1136)

Human mRNA sequence (SEQ ID NO:~~485~~ 1137)

Human coding sequence (SEQ ID NO:~~486~~ 1138)

Table 34 beginning at line 34 of page 58 has been amended as follows:

Table 34 (mouse gene: Nfkbil1; human gene NFKBIL1)

Mouse genomic sequence (SEQ ID NO:~~487~~ 1139)

Mouse mRNA sequence (SEQ ID NO:~~488~~ 1140)

Mouse coding sequence (SEQ ID NO:~~489~~ 1141)

Human genomic sequence (SEQ ID NO:~~490~~ 1142)

Human mRNA sequence (SEQ ID NO:~~491~~ 1143)

Human coding sequence (SEQ ID NO:~~492~~ 1144)

Table 35 beginning at line 3 of page 59 has been amended as follows:

Table 35 (mouse gene: Flt3; human gene FLT3)

Mouse genomic sequence (SEQ ID NO:~~493~~ 1145)

Mouse mRNA sequence (SEQ ID NO:~~494~~ 1146)

Mouse coding sequence (SEQ ID NO:~~495~~ 1147)

Human genomic sequence (SEQ ID NO:~~496~~ 1148)

Human mRNA sequence (SEQ ID NO:~~497~~ 1149)

Human coding sequence (SEQ ID NO:~~498~~ 1150)

Table 36 beginning at line 11 of page 59 has been amended as follows:

Table 36 (mouse gene: Dntt; human gene DNTT)

Mouse genomic sequence (SEQ ID NO:~~499~~ 1151)

Mouse mRNA sequence (SEQ ID NO:~~200~~ 1152)

Mouse coding sequence (SEQ ID NO:~~201~~ 1153)

Human genomic sequence (SEQ ID NO:~~202~~ 1154)

Human mRNA sequence (SEQ ID NO:~~203~~ 1155)

Human coding sequence (SEQ ID NO:~~204~~ 1156)

Table 37 beginning at line 19 of page 59 has been amended as follows:

Table 37 (mouse gene: Znfn1a1; human gene ZNFN1A1)

Mouse genomic sequence (SEQ ID NO:~~205~~ 1157)

Mouse mRNA sequence (SEQ ID NO:~~206~~ 1158)

Mouse coding sequence (SEQ ID NO:~~207~~ 1159)

Human genomic sequence (SEQ ID NO:~~208~~ 1160)

Human mRNA sequence (SEQ ID NO:~~209~~ 1161)

Human coding sequence (SEQ ID NO:~~210~~ 1162)

Table 38 beginning at line 27 of page 59 has been amended as follows:

Table 38 (mouse gene: Tbx21; human gene TBX21)

Mouse genomic sequence (SEQ ID NO:~~211~~ 1163)

Mouse mRNA sequence (SEQ ID NO:~~212~~ 1164)

Mouse coding sequence (SEQ ID NO:~~213~~ 1165)

Human genomic sequence (SEQ ID NO:244 1166)

Human mRNA sequence (SEQ ID NO:215 1167)

Human coding sequence (SEQ ID NO:216 1168)

Table 39 beginning at line 35 of page 59 has been amended as follows:

Table 39 (mouse gene: Stat5b; human gene STAT5B)

Mouse genomic sequence (SEQ ID NO:247 1169)

Mouse mRNA sequence (SEQ ID NO:248 1170)

Mouse coding sequence (SEQ ID NO:249 1171)

Human genomic sequence (SEQ ID NO:220 1172)

Human mRNA sequence (SEQ ID NO:221 1173)

Human coding sequence (SEQ ID NO:222 1174)

Table 40 beginning at line 4 of page 60 has been amended as follows:

Table 40 (mouse gene: Sema4d; human gene SEMA4D)

Mouse genomic sequence (SEQ ID NO:223 1175)

Mouse mRNA sequence (SEQ ID NO:224 1176)

Mouse coding sequence (SEQ ID NO ~~225~~ 1177)

Human genomic sequence (SEQ ID NO ~~226~~ 1178)

Human mRNA sequence (SEQ ID NO:227 1179)

Human coding sequence (SEQ ID NO:228 1180)

Table 41 beginning at line 12 of page 60 has been amended as follows:

Table 41 (mouse gene: Mdm2; human gene MDM2)

Mouse genomic sequence (SEQ ID NO:229 1181)

Mouse mRNA sequence (SEQ ID NO:230 1182)

Mouse coding sequence (SEQ ID NO:231 1183)

Human genomic sequence (SEQ ID NO:232 1184)

Human mRNA sequence (SEQ ID NO:233 1185)

Human coding sequence (SEQ ID NO:234 1186)

Table 42 beginning at line 20 of page 60 has been amended as follows:

Table 42 (mouse gene: Prlr; human gene PRLR)

Mouse genomic sequence (SEQ ID NO:235 1187)

Mouse mRNA sequence (SEQ ID NO:236 1188)

Mouse coding sequence (SEQ ID NO:237 1189)

Human genomic sequence (SEQ ID NO:238 1190)

Human mRNA sequence (SEQ ID NO:239 1191)

Human coding sequence (SEQ ID NO:240 1192)

Table 43 beginning at line 28 of page 60 has been amended as follows:

Table 43 (mouse gene: Top1; human gene TOP1)

Mouse genomic sequence (SEQ ID NO:241 1193)

Mouse mRNA sequence (SEQ ID NO:242 1194)

Mouse coding sequence (SEQ ID NO:243 1195)

Human genomic sequence (SEQ ID NO:244 1196)

Human mRNA sequence (SEQ ID NO:245 1197)

Human coding sequence (SEQ ID NO:246 1198)

Table 44 beginning at line 36 of page 60 has been amended as follows:

Table 44 (mouse gene: Dusp10; human gene DUSP10)

Mouse genomic sequence (SEQ ID NO:247 1199)

Mouse mRNA sequence (SEQ ID NO:248 1200)

Mouse coding sequence (SEQ ID NO:249 1201)

Human genomic sequence (SEQ ID NO:250 1202)

Human mRNA sequence (SEQ ID NO:251 1203)

Human coding sequence (SEQ ID NO:252 1204)

Table 45 beginning at line 5 of page 61 has been amended as follows:

Table 45 (mouse gene: Fli1; human gene FLI1)

Mouse genomic sequence (SEQ ID NO:253 1205)

Mouse mRNA sequence (SEQ ID NO:254 1206)

Mouse coding sequence (SEQ ID NO:~~255~~ 1207)
Human genomic sequence (SEQ ID NO:~~256~~ 1208)
Human mRNA sequence (SEQ ID NO:~~257~~ 1209)
Human coding sequence (SEQ ID NO:~~258~~ 1210)

Table 46 beginning at line 13 of page 61 has been amended as follows:

Table 46 (mouse gene: Tk2; human gene TK2)
Mouse genomic sequence (SEQ ID NO:~~259~~ 1211)
Mouse mRNA sequence (SEQ ID NO:~~260~~ 1212)
Mouse coding sequence (SEQ ID NO:~~264~~ 1213)
Human genomic sequence (SEQ ID NO:~~262~~ 1214)
Human mRNA sequence (SEQ ID NO:~~263~~ 1215)
Human coding sequence (SEQ ID NO:~~264~~ 1216)

Table 47 beginning at line 21 of page 61 has been amended as follows:

Table 47 (mouse gene: Nupr1)
Mouse genomic sequence (SEQ ID NO:~~265~~ 1217)
Mouse mRNA sequence (SEQ ID NO:~~266~~ 1218)
Mouse coding sequence (SEQ ID NO:~~267~~ 1219)
Human genomic sequence (SEQ ID NO:~~268~~ 1220)
Human mRNA sequence (SEQ ID NO:~~269~~ 1221)
Human coding sequence (SEQ ID NO:~~270~~ 1222)

Table 48 beginning at line 29 of page 61 has been amended as follows:

Table 48 (mouse gene: Zfhx1b; human gene ZFHX1B)
Mouse genomic sequence (SEQ ID NO:~~274~~ 1223)
Mouse mRNA sequence (SEQ ID NO:~~272~~ 1224)
Mouse coding sequence (SEQ ID NO:~~273~~ 1225)
Human genomic sequence (SEQ ID NO:~~274~~ 1226)
Human mRNA sequence (SEQ ID NO:~~275~~ 1227)
Human coding sequence (SEQ ID NO:~~276~~ 1228)

Table 49 beginning at line 37 of page 61 has been amended as follows:

Table 49 (mouse gene: Vdac1; human gene VDAC1)

Mouse genomic sequence (SEQ ID NO:~~277~~ 1229)

Mouse mRNA sequence (SEQ ID NO:~~278~~ 1230)

Mouse coding sequence (SEQ ID NO:~~279~~ 1231)

Human genomic sequence (SEQ ID NO:~~280~~ 1232)

Human mRNA sequence (SEQ ID NO:~~281~~ 1233)

Human coding sequence (SEQ ID NO:~~282~~ 1234)

Table 50 beginning at line 6 of page 62 has been amended as follows:

Table 50 (mouse gene: Nfatc1; human gene NFATC1)

Mouse genomic sequence (SEQ ID NO:~~283~~ 1235)

Mouse mRNA sequence (SEQ ID NO:~~284~~ 1236)

Mouse coding sequence (SEQ ID NO:~~285~~ 1237)

Human genomic sequence (SEQ ID NO:~~286~~ 1238)

Human mRNA sequence (SEQ ID NO:~~287~~ 1239)

Human coding sequence (SEQ ID NO:~~288~~ 1240)

Table 51 beginning at line 14 of page 62 has been amended as follows:

Table 51 (mouse gene: Syk; human gene SYK)

Mouse genomic sequence (SEQ ID NO:~~289~~ 1241)

Mouse mRNA sequence (SEQ ID NO:~~290~~ 1242)

Mouse coding sequence (SEQ ID NO:~~291~~ 1243)

Human genomic sequence (SEQ ID NO:~~292~~ 1244)

Human mRNA sequence (SEQ ID NO:~~293~~ 1245)

Human coding sequence (SEQ ID NO:~~294~~ 1246)

Table 52 beginning at line 22 of page 62 has been amended as follows:

Table 52 (mouse gene: Gnb1; human gene GNB1)

Mouse genomic sequence (SEQ ID NO:~~295~~ 1247)

Mouse mRNA sequence (SEQ ID NO:296 1248)
Mouse coding sequence (SEQ ID NO:297 1249)
Human genomic sequence (SEQ ID NO:298 1250)
Human mRNA sequence (SEQ ID NO:299 1251)
Human coding sequence (SEQ ID NO:300 1252).

Table 53 beginning at line 30 of page 62 has been amended as follows:

Table 53 (mouse gene: Ccnd2; human gene CCND2)

Mouse genomic sequence (SEQ ID NO:301 1253)
Mouse mRNA sequence (SEQ ID NO:302 1254)
Mouse coding sequence (SEQ ID NO:303 1255)
Human genomic sequence (SEQ ID NO:304 1256)
Human mRNA sequence (SEQ ID NO:305 1257)
Human coding sequence (SEQ ID NO:306 1258)

Table 54 beginning at line 38 of page 62 has been amended as follows:

Table 54 (mouse gene Tnfrsf6; human gene TNFRSF6)

Mouse genomic sequence (SEQ ID NO:307 1259)
Mouse mRNA sequence (SEQ ID NO:308 1260)
Mouse coding sequence (SEQ ID NO:309 1261)
Human genomic sequence (SEQ ID NO:310 1262)
Human mRNA sequence (SEQ ID NO:311 1263)
Human coding sequence (SEQ ID NO:312 1264)

Table 55 beginning at line 7 of page 63 has been amended as follows:

Table 55 (mouse gene Irf2; human gene IRF2)

Mouse genomic sequence (SEQ ID NO:313 1265)
Mouse mRNA sequence (SEQ ID NO:314 1266)
Mouse coding sequence (SEQ ID NO:315 1267)
Human genomic sequence (SEQ ID NO:316 1268)
Human mRNA sequence (SEQ ID NO:317 1269)

Human coding sequence (SEQ ID NO:318 1270)

Table 56 beginning at line 15 of page 63 has been amended as follows:

Table 56 (mouse gene Morf; human gene: MORF)

Mouse genomic sequence (SEQ ID NO:319 1271)

Mouse mRNA sequence (SEQ ID NO:320 1272)

Mouse coding sequence (SEQ ID NO:324 1273)

Human genomic sequence (SEQ ID NO:322 1274)

Human mRNA sequence (SEQ ID NO:323 1275)

Human coding sequence (SEQ ID NO:324 1276)

Table 57 beginning at line 23 of page 63 has been amended as follows:

Table 57 (mouse gene: Runx3; human gene: RUNX3)

Mouse genomic sequence (SEQ ID NO:325 1277)

Mouse mRNA sequence (SEQ ID NO:326 1278)

Mouse coding sequence (SEQ ID NO:327 1279)

Human genomic sequence (SEQ ID NO:328 1280)

Human mRNA sequence (SEQ ID NO:329 1281)

Human coding sequence (SEQ ID NO:330 1282)

Table 58 beginning at line 31 of page 63 has been amended as follows:

Table 58 (mouse gene: Bcl11b; human gene: BCL11B)

Mouse genomic sequence (SEQ ID NO:334 1283)

Mouse mRNA sequence (SEQ ID NO:332 1284)

Mouse coding sequence (SEQ ID NO:333 1285)

Human genomic sequence (SEQ ID NO:334 1286)

Human mRNA sequence (SEQ ID NO:335 1287)

Human coding sequence (SEQ ID NO:336 1288)

Table 59 beginning at line 39 of page 63 has been amended as follows:

Table 59 (mouse gene: Arhgef1; human gene: ARHGEF1)

Mouse genomic sequence (SEQ ID NO:337 1289)

Mouse mRNA sequence (SEQ ID NO:338 1290)

Mouse coding sequence (SEQ ID NO:339 1291)

Human genomic sequence (SEQ ID NO:340 1292)

Human mRNA sequence (SEQ ID NO:341 1293)

Human coding sequence (SEQ ID NO:342 1294)

Table 60 beginning at line 8 of page 64 has been amended as follows:

Table 60 (mouse gene: Ptpk; human gene: PTPRK)

Mouse genomic sequence (SEQ ID NO:343 1295)

Mouse mRNA sequence (SEQ ID NO:344 1296)

Mouse coding sequence (SEQ ID NO:345 1297)

Human genomic sequence (SEQ ID NO:346 1298)

Human mRNA sequence (SEQ ID NO:347 1299)

Human coding sequence (SEQ ID NO:348 1300)

Table 61 beginning at line 16 of page 64 has been amended as follows:

Table 61 (mouse gene: Mcmd5; human gene: MCM5)

Mouse genomic sequence (SEQ ID NO:349 1301)

Mouse mRNA sequence (SEQ ID NO:350 1302)

Mouse coding sequence (SEQ ID NO:351 1303)

Human genomic sequence (SEQ ID NO:352 1304)

Human mRNA sequence (SEQ ID NO:353 1305)

Human coding sequence (SEQ ID NO:354 1306)

Table 62 beginning at line 24 of page 64 has been amended as follows:

Table 62 (mouse gene: Matn4; human gene: MATN4)

Mouse genomic sequence (SEQ ID NO:355 1307)

Mouse mRNA sequence (SEQ ID NO:356 1308)

Mouse coding sequence (SEQ ID NO:357 1309)

Human genomic sequence (SEQ ID NO:358 1310)

Human mRNA sequence (SEQ ID NO:~~359~~ 1311)

Human coding sequence (SEQ ID NO:~~360~~ 1312)

Table 63 beginning at line 32 of page 64 has been amended as follows:

Table 63 (mouse gene: Tnfsf11; human gene TNFSF11)

Mouse genomic sequence (SEQ ID NO:~~361~~ 1313)

Mouse mRNA sequence (SEQ ID NO:~~362~~ 1314)

Mouse coding sequence (SEQ ID NO:~~363~~ 1315)

Human genomic sequence (SEQ ID NO:~~364~~ 1316)

Human mRNA sequence (SEQ ID NO:~~365~~ 1317)

Human coding sequence (SEQ ID NO:~~366~~ 1318)

Table 64 beginning at line 1 of page 65 has been amended as follows:

Table 64 (mouse gene: Itk; human gene ITK)

Mouse genomic sequence (SEQ ID NO:~~367~~ 1319)

Mouse mRNA sequence (SEQ ID NO:~~368~~ 1320)

Mouse coding sequence (SEQ ID NO:~~369~~ 1321)

Human genomic sequence (SEQ ID NO:~~370~~ 1322)

Human mRNA sequence (SEQ ID NO:~~371~~ 1323)

Human coding sequence (SEQ ID NO:~~372~~ 1324)

Table 65 beginning at line 9 of page 65 has been amended as follows:

Table 65 (mouse gene: Fish; human gene: N/A)

Mouse genomic sequence (SEQ ID NO:~~373~~ 1325)

Mouse mRNA sequence (SEQ ID NO:~~374~~ 1326)

Mouse coding sequence (SEQ ID NO:~~375~~ 1327)

Human genomic sequence (SEQ ID NO:~~376~~ 1328)

Human mRNA sequence (SEQ ID NO:~~377~~ 1329)

Human coding sequence (SEQ ID NO:~~378~~ 1330)

Table 66 beginning at line 17 of page 65 has been amended as follows:

Table 66 (mouse gene: Egr2; human gene EGR2)

Mouse genomic sequence (SEQ ID NO:~~379~~ 1331)

Mouse mRNA sequence (SEQ ID NO:~~380~~ 1332)

Mouse coding sequence (SEQ ID NO:~~384~~ 1333)

Human genomic sequence (SEQ ID NO:~~382~~ 1334)

Human mRNA sequence (SEQ ID NO:~~383~~ 1335)

Human coding sequence (SEQ ID NO:~~384~~ 1336)

Table 67 beginning at line 25 of page 65 has been amended as follows:

Table 67 (mouse gene: Sos1; human gene SOS1)

Mouse genomic sequence (SEQ ID NO:~~385~~ 1337)

Mouse mRNA sequence (SEQ ID NO:~~386~~ 1338)

Mouse coding sequence (SEQ ID NO:~~387~~ 1339)

Human genomic sequence (SEQ ID NO:~~388~~ 1340)

Human mRNA sequence (SEQ ID NO:~~389~~ 1341)

Human coding sequence (SEQ ID NO:~~390~~ 1342)

Table 68 beginning at line 33 of page 65 has been amended as follows:

Table 68 (mouse gene: Pou2af1; human gene POU2AF1)

Mouse genomic sequence (SEQ ID NO:~~391~~ 1343)

Mouse mRNA sequence (SEQ ID NO:~~392~~ 1344)

Mouse coding sequence (SEQ ID NO:~~393~~ 1345)

Human genomic sequence (SEQ ID NO:~~394~~ 1346)

Human mRNA sequence (SEQ ID NO:~~395~~ 1347)

Human coding sequence (SEQ ID NO:~~396~~ 1348)

Table 69 beginning at line 1 of page 66 has been amended as follows:

Table 69 (mouse gene: Mef2c; human gene MEF2C)

Mouse genomic sequence (SEQ ID NO:~~397~~ 1349)

Mouse mRNA sequence (SEQ ID NO:~~398~~ 1350)

Mouse coding sequence (SEQ ID NO:~~399~~ 1351)

Human genomic sequence (SEQ ID NO:400 1352)

Human mRNA sequence (SEQ ID NO:401 1353)

Human coding sequence (SEQ ID NO:402 1354)

Table 70 beginning at line 10 of page 66 has been amended as follows:

Table 70 (mouse gene: Map3k8; human gene MAP3K8)

Mouse genomic sequence (SEQ ID NO:403 1355)

Mouse mRNA sequence (SEQ ID NO:404 1356)

Mouse coding sequence (SEQ ID NO:405 1357)

Human genomic sequence (SEQ ID NO:406 1358)

Human mRNA sequence (SEQ ID NO:407 1359)

Human coding sequence (SEQ ID NO:408 1360)

Table 71 beginning at line 18 of page 66 has been amended as follows:

Table 71 (mouse gene: Fgfr3; human gene FGFR3)

Mouse genomic sequence (SEQ ID NO:409 1361)

Mouse mRNA sequence (SEQ ID NO:410 1362)

Mouse coding sequence (SEQ ID NO:411 1363)

Human genomic sequence (SEQ ID NO:412 1364)

Human mRNA sequence (SEQ ID NO:413 1365)

Human coding sequence (SEQ ID NO:414 1366)

Table 72 beginning at line 26 of page 66 has been amended as follows:

Table 72 (mouse gene: Cbx8; human gene CBX8)

Mouse genomic sequence (SEQ ID NO:415 1367)

Mouse mRNA sequence (SEQ ID NO:416 1368)

Mouse coding sequence (SEQ ID NO:417 1369)

Human genomic sequence (SEQ ID NO:418 1370)

Human mRNA sequence (SEQ ID NO:419 1371)

Human coding sequence (SEQ ID NO:420 1372)

Table 73 beginning at line 34 of page 66 has been amended as follows:

Table 73 (mouse gene: Lmo2; human gene LMO2)

Mouse genomic sequence (SEQ ID NO:424 1373)

Mouse mRNA sequence (SEQ ID NO:422 1374)

Mouse coding sequence (SEQ ID NO:423 1375)

Human genomic sequence (SEQ ID NO:424 1376)

Human mRNA sequence (SEQ ID NO:425 1377)

Human coding sequence (SEQ ID NO:426 1378)

Table 74 beginning at line 3 of page 67 has been amended as follows:

Table 74 (mouse gene: Itpr1; human gene ITPR1)

Mouse genomic sequence (SEQ ID NO:427 1379)

Mouse mRNA sequence (SEQ ID NO:428 1380)

Mouse coding sequence (SEQ ID NO:429 1381)

Human genomic sequence (SEQ ID NO:430 1382)

Human mRNA sequence (SEQ ID NO:431 1383)

Human coding sequence (SEQ ID NO:432 1384)

Table 75 beginning at line 11 of page 67 has been amended as follows:

Table 75 (mouse gene: Sell; human gene SELL)

Mouse genomic sequence (SEQ ID NO:433 1385)

Mouse mRNA sequence (SEQ ID NO:434 1386)

Mouse coding sequence (SEQ ID NO:435 1387)

Human genomic sequence (SEQ ID NO:436 1388)

Human mRNA sequence (SEQ ID NO:437 1389)

Human coding sequence (SEQ ID NO:438 1390)

Table 76 beginning at line 19 of page 67 has been amended as follows:

Table 76 (mouse gene: Dpt; human gene DPT)

Mouse genomic sequence (SEQ ID NO:439 1391)

Mouse mRNA sequence (SEQ ID NO:440 1392)

Mouse coding sequence (SEQ ID NO:444 1393)
Human genomic sequence (SEQ ID NO:442 1394)
Human mRNA sequence (SEQ ID NO:443 1395)
Human coding sequence (SEQ ID NO:444 1396)

Table 77 beginning at line 27 of page 67 has been amended as follows:

Table 77 (mouse gene: Pap; human gene PAP)
Mouse genomic sequence (SEQ ID NO:445 1397)
Mouse mRNA sequence (SEQ ID NO:446 1398)
Mouse coding sequence (SEQ ID NO:447 1399)
Human genomic sequence (SEQ ID NO:448 1400)
Human mRNA sequence (SEQ ID NO:449 1401)
Human coding sequence (SEQ ID NO:450 1402)

Table 78 beginning at line 35 of page 67 has been amended as follows:

Table 78 (mouse gene: Blm; human gene BLM)
Mouse genomic sequence (SEQ ID NO:451 1403)
Mouse mRNA sequence (SEQ ID NO:452 1404)
Mouse coding sequence (SEQ ID NO:453 1405)
Human genomic sequence (SEQ ID NO:454 1406)
Human mRNA sequence (SEQ ID NO:455 1407)
Human coding sequence (SEQ ID NO:456 1408)

Table 79 beginning at line 4 of page 68 has been amended as follows:

Table 79 (mouse gene: Blr1; human gene BLR1)
Mouse genomic sequence (SEQ ID NO:457 1409)
Mouse mRNA sequence (SEQ ID NO:458 1410)
Mouse coding sequence (SEQ ID NO:459 1411)
Human genomic sequence (SEQ ID NO:460 1412)
Human mRNA sequence (SEQ ID NO:461 1413)
Human coding sequence (SEQ ID NO:462 1414)

Table 80 beginning at line 12 of page 68 has been amended as follows:

Table 80 (mouse gene: Ptp4a2; human gene PTP4A2)

Mouse genomic sequence (SEQ ID NO:~~463~~ 1415)

Mouse mRNA sequence (SEQ ID NO:~~464~~ 1416)

Mouse coding sequence (SEQ ID NO:~~465~~ 1417)

Human genomic sequence (SEQ ID NO:~~466~~ 1418)

Human mRNA sequence (SEQ ID NO:~~467~~ 1419)

Human coding sequence (SEQ ID NO:~~468~~ 1420)

Table 81 beginning at line 20 of page 68 has been amended as follows:

Table 81 (mouse gene: Mcm3ap; human gene MCM3AP)

Mouse genomic sequence (SEQ ID NO:~~469~~ 1421)

Mouse mRNA sequence (SEQ ID NO:~~470~~ 1422)

Mouse coding sequence (SEQ ID NO:~~471~~ 1423)

Human genomic sequence (SEQ ID NO:~~472~~ 1424)

Human mRNA sequence (SEQ ID NO:~~473~~ 1425)

Human coding sequence (SEQ ID NO:~~474~~ 1426)

Table 82 beginning at line 28 of page 68 has been amended as follows:

Table 82 (mouse gene: Jak2; human gene JAK2)

Mouse genomic sequence (SEQ ID NO:~~475~~ 1427)

Mouse mRNA sequence (SEQ ID NO:~~476~~ 1428)

Mouse coding sequence (SEQ ID NO:~~477~~ 1429)

Human genomic sequence (SEQ ID NO:~~478~~ 1430)

Human mRNA sequence (SEQ ID NO:~~479~~ 1431)

Human coding sequence (SEQ ID NO:~~480~~ 1432)

Table 83 beginning at line 36 of page 68 has been amended as follows:

Table 83 (mouse gene: Fus1; human gene FUS1)

Mouse genomic sequence (SEQ ID NO:~~481~~ 1433)

Mouse mRNA sequence (SEQ ID NO:482 1434)
Mouse coding sequence (SEQ ID NO:483 1435)
Human genomic sequence (SEQ ID NO:484 1436)
Human mRNA sequence (SEQ ID NO:485 1437)
Human coding sequence (SEQ ID NO:486 1438)

Table 84 beginning at line 5 of page 69 has been amended as follows:

Table 84 (mouse gene: Rassf1; human gene RASSF1)

Mouse genomic sequence (SEQ ID NO:487 1439)
Mouse mRNA sequence (SEQ ID NO:488 1440)
Mouse coding sequence (SEQ ID NO:489 1441)
Human genomic sequence (SEQ ID NO:490 1442)
Human mRNA sequence (SEQ ID NO:491 1443)
Human coding sequence (SEQ ID NO:492 1444)

Table 85 beginning at line 13 of page 69 has been amended as follows:

Table 85 (mouse gene: Pik3r1; human gene PIK3R1)

Mouse genomic sequence (SEQ ID NO:493 1445)
Mouse mRNA sequence (SEQ ID NO:494 1446)
Mouse coding sequence (SEQ ID NO:495 1447)
Human genomic sequence (SEQ ID NO:496 1448)
Human mRNA sequence (SEQ ID NO:497 1449)
Human coding sequence (SEQ ID NO:498 1450)

Table 86 beginning at line 21 of page 69 has been amended as follows:

Table 86 (mouse gene: Braf; human gene BRAF)

Mouse genomic sequence (SEQ ID NO:499 1451)
Mouse mRNA sequence (SEQ ID NO:500 1452)
Mouse coding sequence (SEQ ID NO:501 1453)
Human genomic sequence (SEQ ID NO:502 1454)
Human mRNA sequence (SEQ ID NO:503 1455)

Human coding sequence (SEQ ID NO:~~504~~ 1456)

Table 87 beginning at line 29 of page 69 has been amended as follows:

Table 87 (mouse gene: Tle3; human gene: TLE3)

Mouse genomic sequence (SEQ ID NO:~~505~~ 1457)

Mouse mRNA sequence (SEQ ID NO:~~506~~ 1458)

Mouse coding sequence (SEQ ID NO:~~507~~ 1459)

Human genomic sequence (SEQ ID NO:~~508~~ 1460)

Human mRNA sequence (SEQ ID NO:~~509~~ 1461)

Human coding sequence (SEQ ID NO:~~510~~ 1462)

Table 88 beginning at line 37 of page 69 has been amended as follows:

Table 88 (mouse gene: Nek2; human gene NEK2)

Mouse genomic sequence (SEQ ID NO:~~511~~ 1463)

Mouse mRNA sequence (SEQ ID NO:~~512~~ 1464)

Mouse coding sequence (SEQ ID NO:~~513~~ 1465)

Human genomic sequence (SEQ ID NO:~~514~~ 1466)

Human mRNA sequence (SEQ ID NO:~~515~~ 1467)

Human coding sequence (SEQ ID NO:~~516~~ 1468)

Table 89 beginning at line 6 of page 70 has been amended as follows:

Table 89 (mouse gene: Nr3c1; human gene NR3C1)

Mouse genomic sequence (SEQ ID NO: ~~517~~ 1469)

Mouse mRNA sequence (SEQ ID NO:~~518~~ 1470)

Mouse coding sequence (SEQ ID NO:~~519~~ 1471)

Human genomic sequence (SEQ ID NO:~~520~~ 1472)

Human mRNA sequence (SEQ ID NO: ~~521~~ 1473)

Human coding sequence (SEQ ID NO:~~522~~ 1474)

Table 90 beginning at line 14 of page 70 has been amended as follows:

Table 90 (mouse gene: Dad1; human gene DAD1)

Mouse genomic sequence (SEQ ID NO:~~523~~ 1475)
Mouse mRNA sequence (SEQ ID NO:~~524~~ 1476)
Mouse coding sequence (SEQ ID NO:~~525~~ 1477)
Human genomic sequence (SEQ ID NO:~~526~~ 1478)
Human mRNA sequence (SEQ ID NO:~~527~~ 1479)
Human coding sequence (SEQ ID NO:~~528~~ 1480)

Table 91 beginning at line 22 of page 70 has been amended as follows:

Table 91 (mouse gene: Lck; human gene LCK)
Mouse genomic sequence (SEQ ID NO:~~529~~ 1481)
Mouse mRNA sequence (SEQ ID NO:~~530~~ 1482)
Mouse coding sequence (SEQ ID NO:~~531~~ 1483)
Human genomic sequence (SEQ ID NO:~~532~~ 1484)
Human mRNA sequence (SEQ ID NO:~~533~~ 1485)
Human coding sequence (SEQ ID NO:~~534~~ 1486)

Table 92 beginning at line 30 of page 70 has been amended as follows:

Table 92 (mouse gene: Git2; human gene GIT2)
Mouse genomic sequence (SEQ ID NO:~~535~~ 1487)
Mouse mRNA sequence (SEQ ID NO:~~536~~ 1488)
Mouse coding sequence (SEQ ID NO:~~537~~ 1489)
Human genomic sequence (SEQ ID NO:~~538~~ 1490)
Human mRNA sequence (SEQ ID NO:~~539~~ 1491)
Human coding sequence (SEQ ID NO:~~540~~ 1492).

Table 93 beginning at line 38 on page 70 has been amended as follows:

Table 93 (mouse gene: Anp32; human gene N/A)
Mouse genomic sequence (SEQ ID NO:~~541~~ 1493)
Mouse mRNA sequence (SEQ ID NO:~~542~~ 1494)
Mouse coding sequence (SEQ ID NO:~~543~~ 1495)
Human genomic sequence (SEQ ID NO:~~544~~ 1496)

Human mRNA sequence (SEQ ID NO:~~545~~ 1497)

Human coding sequence (SEQ ID NO:~~546~~ 1498).

Table 94 beginning at line 7 of page 71 has been amended as follows:

Table 94 (mouse gene: Map2k5; human gene MAP2K5)

Mouse genomic sequence (SEQ ID NO:~~547~~ 1499)

Mouse mRNA sequence (SEQ ID NO:~~548~~ 1500)

Mouse coding sequence (SEQ ID NO:~~549~~ 1501)

Human genomic sequence (SEQ ID NO:~~550~~ 1502)

Human mRNA sequence (SEQ ID NO:~~551~~ 1503)

Human coding sequence (SEQ ID NO:~~552~~ 1504).

Table 95 beginning at line 15 of pae 71 has been amended as follows:

Table 95 (mouse gene: Cd28; human gene CD28)

Mouse genomic sequence (SEQ ID NO:~~553~~ 1505)

Mouse mRNA sequence (SEQ ID NO:~~554~~ 1506)

Mouse coding sequence (SEQ ID NO:~~555~~ 1507)

Human genomic sequence (SEQ ID NO:~~556~~ 1508)

Human mRNA sequence (SEQ ID NO: ~~556~~ 1509)

Human coding sequence (SEQ ID NO:~~558~~ 1510).

Table 96 beginning at line 23 of page 71 has been amended as follows:

Table 96 (mouse gene: Sept9; human gene Msf)

Mouse genomic sequence (SEQ ID NO:~~559~~ 1511)

Mouse mRNA sequence (SEQ ID NO:~~560~~ 1512)

Mouse coding sequence (SEQ ID NO:~~561~~ 1513)

Human genomic sequence (SEQ ID NO:~~562~~ 1514)

Human mRNA sequence (SEQ ID NO:~~563~~ 1515)

Human coding sequence (SEQ ID NO:~~564~~ 1516).

Table 97 beginning at line 31 of page 71 has been amended as follows:

Table 97 (mouse gene: Fzd10; human gene FZD10)

Mouse genomic sequence (SEQ ID NO:~~565~~ 1517)

Mouse mRNA sequence (SEQ ID NO:~~566~~ 1518)

Mouse coding sequence (SEQ ID NO:~~567~~ 1519)

Human genomic sequence (SEQ ID NO:~~568~~ 1520)

Human mRNA sequence (SEQ ID NO:~~569~~ 1521)

Human coding sequence (SEQ ID NO:~~570~~ 1522).

Table 98 beginning at line 39 of page 71 has been amended as follows:

Table 98 (mouse gene: Calm2; human gene CALM2)

Mouse genomic sequence (SEQ ID NO:~~571~~ 1523)

Mouse mRNA sequence (SEQ ID NO:~~572~~ 1524)

Mouse coding sequence (SEQ ID NO:~~573~~ 1525)

Human genomic sequence (SEQ ID NO:~~574~~ 1526)

Human mRNA sequence (SEQ ID NO:~~575~~ 1527)

Human coding sequence (SEQ ID NO:~~576~~ 1528).

Table 99 beginning at line 8 of page 72 has been amended as follows:

Table 99 (mouse gene: Ncf4; human gene NCF4)

Mouse genomic sequence (SEQ ID NO:~~577~~ 1529)

Mouse mRNA sequence (SEQ ID NO:~~578~~ 1530)

Mouse coding sequence (SEQ ID NO:~~579~~ 1531)

Human genomic sequence (SEQ ID NO:~~580~~ 1532)

Human mRNA sequence (SEQ ID NO:~~581~~ 1533)

Human coding sequence (SEQ ID NO:~~582~~ 1534).

Table 100 beginning at line 16 of page 72 has been amended as follows:

Table 100 (mouse gene: Rac2; human gene RAC2)

Mouse genomic sequence (SEQ ID NO:~~583~~ 1535)

Mouse mRNA sequence (SEQ ID NO:~~584~~ 1536)
Mouse coding sequence (SEQ ID NO:~~585~~ 1537)
Human genomic sequence (SEQ ID NO:~~586~~ 1538)
Human mRNA sequence (SEQ ID NO:~~587~~ 1539)
Human coding sequence (SEQ ID NO:~~588~~ 1540).

Table 101 beginning at line 24 of page 72 has been amended as follows:

Table 101 (mouse gene: Mbnl; human gene MBNL)

Mouse genomic sequence (SEQ ID NO:~~589~~ 1541)
Mouse mRNA sequence (SEQ ID NO:~~590~~ 1542)
Mouse coding sequence (SEQ ID NO:~~591~~ 1543)
Human genomic sequence (SEQ ID NO:~~592~~ 1544)
Human mRNA sequence (SEQ ID NO:~~593~~ 1545)
Human coding sequence (SEQ ID NO:~~594~~ 1546).

Table 102 beginning at line 32 of page 72 has been amended as follows:

Table 102 (mouse gene: mCG10516; human gene N/A)

Mouse genomic sequence (SEQ ID NO:~~595~~ 1547)
Mouse mRNA sequence (SEQ ID NO:~~596~~ 1548)
Mouse coding sequence (SEQ ID NO:~~597~~ 1549)
Human genomic sequence (SEQ ID NO:~~598~~ 1550)
Human mRNA sequence (SEQ ID NO:~~599~~ 1551)
Human coding sequence (SEQ ID NO:~~600~~ 1552)

Table 103 beginning at line 1 of page 73 has been amended as follows:

Table 103 (mouse gene: Rorc; human gene RORC)

Mouse genomic sequence (SEQ ID NO:~~601~~ 1553)
Mouse mRNA sequence (SEQ ID NO:~~602~~ 1554)
Mouse coding sequence (SEQ ID NO:~~603~~ 1555)
Human genomic sequence (SEQ ID NO:~~604~~ 1556)
Human mRNA sequence (SEQ ID NO:~~605~~ 1557)

Human coding sequence (SEQ ID NO:606 1558)

Table 104 beginning at line 9 of page 73 has been amended as follows:

Table 104 (mouse gene mCG15938; human gene BAT1)

Mouse genomic sequence (SEQ ID NO:607 1559)

Mouse mRNA sequence (SEQ ID NO:608 1560)

Mouse coding sequence (SEQ ID NO:609 1561)

Human genomic sequence (SEQ ID NO:640 1562)

Human mRNA sequence (SEQ ID NO:641 1563)

Human coding sequence (SEQ ID NO:642 1564)

Table 105 beginning at line 17 of page 73 has been amended as follows:

Table 105 (mouse gene: Iqgap1; human gene IQGAP1)

Mouse genomic sequence (SEQ ID NO:643 1565)

Mouse mRNA sequence (SEQ ID NO:644 1566)

Mouse coding sequence (SEQ ID NO:645 1567)

Human genomic sequence (SEQ ID NO:646 1568)

Human mRNA sequence (SEQ ID NO:647 1569)

Human coding sequence (SEQ ID NO:648 1570)

Table 106 beginning at line 25 of page 73 has been amended as follows:

Table 106 (mouse gene Zpf29; human gene: hCG27579)

Mouse genomic sequence (SEQ ID NO:649 1571)

Mouse mRNA sequence (SEQ ID NO:620 1572)

Mouse coding sequence (SEQ ID NO:624 1573)

Human genomic sequence (SEQ ID NO:622 1574)

Human mRNA sequence (SEQ ID NO:623 1575)

Human coding sequence (SEQ ID NO:624 1576)

Table 107 beginning at line 33 of page 73 has been amended as follows:

Table 107 (mouse gene: Kcnj9; human gene: KCNJ9)

Mouse genomic sequence (SEQ ID NO:625 1577)

Mouse mRNA sequence (SEQ ID NO:626 1578)

Mouse coding sequence (SEQ ID NO:627 1579)

Human genomic sequence (SEQ ID NO:628 1580)

Human mRNA sequence (SEQ ID NO:629 1581)

Human coding sequence (SEQ ID NO:630 1582)

Table 108 beginning at line 1 of page 74 has been amended as follows:

Table 108 (mouse gene: Ppp3cc; human gene: PPP3CC)

Mouse genomic sequence (SEQ ID NO:634 1583)

Mouse mRNA sequence (SEQ ID NO:632 1584)

Mouse coding sequence (SEQ ID NO:633 1585)

Human genomic sequence (SEQ ID NO:634 1586)

Human mRNA sequence (SEQ ID NO:635 1587)

Human coding sequence (SEQ ID NO:636 1588)

Table 109 beginning at line 9 of page 74 has been amended as follows:

Table 109 (mouse gene: mCG9110; human gene: hCG27579)

Mouse genomic sequence (SEQ ID NO:637 1589)

Mouse mRNA sequence (SEQ ID NO:638 1590)

Mouse coding sequence (SEQ ID NO:639 1591)

Human genomic sequence (SEQ ID NO:640 1592)

Human mRNA sequence (SEQ ID NO:641 1593)

Human coding sequence (SEQ ID NO:642 1594)

Table 110 beginning at line 17 of page 74 has been amended as follows:

Table 110 (mouse gene: mCG2257; human gene: PRDM11)

Mouse genomic sequence (SEQ ID NO:643 1595)

Mouse mRNA sequence (SEQ ID NO:644 1596)

Mouse coding sequence (SEQ ID NO:645 1597)

Human genomic sequence (SEQ ID NO:646 1598)

Human mRNA sequence (SEQ ID NO:~~647~~ 1599)

Human coding sequence (SEQ ID NO:~~648~~ 1600)

Table 111 beginning at line 25 of page 74 has been amended as follows:

Table 111 (mouse gene: mCG17918; human gene: hCG23764)

Mouse genomic sequence (SEQ ID NO:~~649~~ 1601)

Mouse mRNA sequence (SEQ ID NO:~~650~~ 1602)

Mouse coding sequence (SEQ ID NO:~~654~~ 1603)

Human genomic sequence (SEQ ID NO:~~652~~ 1604)

Human mRNA sequence (SEQ ID NO:~~653~~ 1605)

Human coding sequence (SEQ ID NO:~~654~~ 1606)

Table 112 beginning at line 33 of page 74 has been amended as follows:

Table 112 (mouse gene: Lfng; human gene: LFNG)

Mouse genomic sequence (SEQ ID NO:~~655~~ 1607)

Mouse mRNA sequence (SEQ ID NO:~~656~~ 1608)

Mouse coding sequence (SEQ ID NO:~~657~~ 1609)

Human genomic sequence (SEQ ID NO:~~658~~ 1610)

Human mRNA sequence (SEQ ID NO:~~659~~ 1611)

Human coding sequence (SEQ ID NO:~~660~~ 1612).

Table 1

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>1</u>	IM000619	GATCAAAGCAATCTCTATGTCTTTCTCTG CTGTCCTCCTCAGACATCTCCAGAGAGC TGGGATATTTTTCTTTCCATTGAGATT ATGAAGTTGTTTCTAGAGTGCATGACGC AGGTTGAAGGATAAGTACACAGGTCCCA AGGAACCAAGCGTTTTCACTGACGGTGA TGAGTCTTGTTCTGTGAGATTGTTGTGATT CTCAGCCTTTCTCTTCCCCTGTGTGTGCT CTTCATTTTCTGGTTCTGTCTGCCTAGCA CCTCCTGGGGAAGCTGCTGTGCTTT	p000632	A	<i>Spr</i>
<u>2</u>	IM000620	GATCTTTGAGCCCAGTTGTTAATCATAA GAGCTGATATTTTGAAGAGTGTGTCAA CCTAGATGCACAGGGAAGCCAAAGCATT CAGCC	p000633	D	--
<u>3</u>	IM000621	ATATGACCACAAGGAAATAAGATAAAGT GTTCATACTGAATTTATAATGAAAAGTGA TC	p000634	C	--
<u>4</u>	IM000622	GAACAGGCATGGCTTTACTTGTACAATG AGGAAACCAAGGCAGAGATTGCAAAGCG GGTCCTACACGTTTGCTCCATGCCCTGC TTCTCTGACCACAGTGTACTGAGAATATG CTGAGCCCTAGTTCCTGGGGAGGAGGC AGAAGAGAGCAGCATCCTGCCCACTTGA AGGCGTGCACACATAGTTCCTGTCTGAT C	p000638	D	--
<u>5</u>	IM000623	GATCAGGAGACCACACCCAGCTAGCCTT CTCTGACTGGGTATCCTTGGTCAGCCAG CCTTTCTTCACCTCATGTTCTCATTTGCA AACTCACATGAACACTATTTGACCTACAC ACTTCATAAAGCTGTTTTTAGAAAGACGA GATAATACAGGAGGAACGCTACAATATT AAATGATATGTATTTATAT	p000639	D	--
<u>6</u>	IM000624	AGTGTTTAGGTCAGCTGGTGCAGGAGAA GCTTCTTGAGGAAGACGACCATCTGGCA AGGCCTGATGGTAGAAAATAATGGACTT CTCTCCAAGTGAAGTAGGAAGTTGATGAT C	p000640	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>7</u>	IM000625	ATCAGTAAGTTAATCCTAAGAATTACTAT GCATTTTTCCCCTCTTTTTTAACAACATT CTCCTTAGCTTATATGAGGCTCTAGTGC CCGGAGACTTTAATACTGCCCTAACATG ATGGTGGCTCTTTGTCCCTCTTTCTCAGC CACTGAAATCTGACAGTTTGGGAAGAA TAATAAGAATTTAAGAACTAGATGGTTT TAAATATAGATATAAAAACAGTTCTTCGA CTATTCTCAATAAAGAAATTCAGTCAAAA GAATTCAGTCCTAACACAATGATC	p000641	D	--
<u>8</u>	IM000626	GATCATCAGAGTCCTGCATCTTATGTGT GCAGTGTTTTCAGCAATACAGGCTTACC TTCAACCTCTAACAGGCAACCAGATGCT ACAATAGCTTATATTGTTTTAGAAATCAC TTGGACTACTCTAAACAACAACTTGAGTG AAGGCTCTTTGTATCTGATACTGGAGTTT GTTAGTCTATGACACTTGTGGGGAGACA TGTCTGCACAAGTAGCATATGTGTGTAC ATGTATATTGTATACATATATAGTTTTGCT CTATGTATGTATGTGTATATGTATGTATG TATATGTATATGTATGTATATATATAG	p000642	D	--
<u>9</u>	IM000627	AAGGGACCTGATAATCGTGTTGGCAACT GGGCTACAATTAGTTATCAATTGCTTGCT TGCCACCTGCCCTGCTCCATAGAGAATC ATAGTCTGGGGAGTGTGGAGGAATAGC GGAGTCATCTAAACACATCACTGCTGCC CCCACCATTTGCCTGCCACCAGGCCCTT GCCTTTTCATTTTGCATTTCTCCCTCTTAC AAGCAAATGGCGCTCACTGATC	p000643	D	--
<u>10</u>	IM000628	GTTTGGGGATTGTACAGAATGCACAGCG TAGTATTCAGGAAAAAGGAACTGGGAA ATTAATGTATAAATTTAAATCAGCTTTTAA TTAGCTTAACACACACATACGAAGGCAA AAATGTAACGTTACTTTGATC	p000644	K	<i>Myc</i>
<u>11</u>	IM000629	GATCTCATTACAGATGGTTGTGAGCTAC CATGTGG	p000647	R	--
<u>12</u>	IM000630	GATCTCAGGAGGCACCGAGAGACTCAG CATGGACTCAAATGAGTACCCTGGCAGC CCGCAACACCAGCTGTGTAACACTACCG TGAGGGATGTCTTCCCTGCCTCCCTCCA GCCCCCTTCTCAGGCCCTGAGTCCAGTGT GCAAAGCTCATCATGGTTAGTCCCCTTC ACCT	p000649	K	<i>Gfi1</i>
<u>13</u>	IM000631	AGAGCACCCGACTGCTCTTCCGAAGGTC CAGAGTTCAAATCCCAGCAACCACATGG TGGCTCACAACCATCCGTAACAAGATC	p000650	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>14</u>	IM000632	GATCAAATCCTGTCAGGGAGAGGGGCTC CTCCCAGTAGTGCCATCCCATAATAATAA GAAGGACTCCTGGGCCTCAGTGAAGTCA GGCTGACCACTACTGCAGGTTAGTCATG ACCACTAGCCAGAATGGAACGAAGGGT GACCCAGTGTGAGGACACAGCCCCAGG CAACTGCTTCTGCTTTGAGCCAAGTTGTT ACCCCAAAGCTCGTCATTCCGCTTGGTT TCTCATGTGTGTGAGCTGCACATATGGA GGTCCCCCTTTGTTCCCTT	p000651	D	--
<u>15</u>	IM000633	GTGAGGAAGGTCCCTCTGCATTCTAACC TTCCTCAACTCCACCAGCCTCGGCGTTT AAGGGAGAAATATTACCGTTCCCTTTGG GCCAAGTTGGAGCCAGTGAAGTAGTCG GAAATGTACAGTCACAGGAAATTGCTGC TACCAAGGCTGGAGGAACAAAGAGAAGA CTTGTCACAAGAGGCCAGAGAGGAAGTC ACCCAGTACAACTGAAGCGCGCGCGC ACACACACACACACACACACACACGC ACACACACACACACACGATC	p000652	D	--
<u>16</u>	IM000634	TGGCCGCCTAGACAAGCTGACCATCACC TCCCAGAACCTGCAACTGGAGAGCCTTC GCATGAAGCTTCCGAAATGTGCGTGCTC CACCTGTCCCTCACCTCACAGACATCAT TTCTCCATTTAGCCCCTCCCGATC	p000654	A	<i>li</i>
<u>17</u>	IM000635	GATCCCCTGGAATTTACAGTCGGTTCCA ACAATCATGTAGATG	p000656	C	--
<u>18</u>	IM000636	GATCGGCTATAGCATTGTCAATGTTTAC CCAGAAGAATAGCACAGATATATTGCA CATCAATGCTTATTGCAGTATTATTCACA GTGGCTATGTAATGGAACCAACCTACAT GGCCAGCAACTGAATAGATTAAGAAAAT ATATATACACAATGGTGCTTTTTTCGGCT ATAAAGAAGAATGAAGTTATGTTGTTGT TAGAAGATGGATGAAAGTGGAGATGATA ATATCAAGTGCACAGTCAACCTCTCTCTC TCACCTCCCCCGCCCCGCTCTTTCTCTC TCATATACATTTGAGAGTAGCAGTAACT GTCTGAGAACAAAGGGGATTAATGGGAG GGGAGAAGATTAAGGAGCGGAAGGGTA GTAGGTAGTAT	p000659	A	<i>Cr2</i>
<u>19</u>	IM000637	GATCGGCTTCTATGGACTGAGTGTGTAA GAAAACATT	p000661	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>20</u>	IM000638	TTAGGAGGGTAGAGAACATTCAGGAATC AAGAACAAGCATTTTAACACCCACTGAG CTATCCTGTGGATGGTGGTGGTTTTGTTT GTTTGTTGGTTTTGTTTAGGAAGTCAGG GATGGGGTGGGAATCTCACTCTGTGGCT TAGACTTGCAACAATCCCAAATTCTGGAA TGATAAGCAAGAGAGCTGTCTAGTCCCA GTCTCAGATACATGCTGTTAATTTTCTAC TACTGCTATAACACATAGGCTCAAATGC GGTGGCTTACCTAACACACCCTGTGCAG TTCTGAAAGTCGTAACCTCTGGCACGATC	p000662	D	--
<u>21</u>	IM000639	ATGCTAAGCTGTGACTCCTCTCGATACG AGACCCTGGCTGCCCTCCTTTCCCGATC	p000663	D	--
<u>22</u>	IM000640	GATCGTCTGGAAGAGCAGTCAGTATTCT TAACTGCTGAGCCATCTTTCAGCCCCC AGTTCTTTGGGGTTTTTGTGTTGTTGTT GGTTGGTTGGTTGGTTGGTTAGTTTG GTTTGGTTCAAGACAGGGTTTCTCTGTG TTGCCCTGGATGTCCTGGAACCTCTTT GTAGACCAGGGTGGCCTTTAACTCACAG AAATGCGCCTGCTAGGATTAAAGCTGTG TCCCACCACTATATATATATGTGTG	p000665	R	--
<u>23</u>	IM000641	GTCACAGTGTTAGAGCCACAGACGGGG GAACCTACTGGCTGTCCTGGGTTCTGT AAACTAGGGGACAAAGCTGCCACAGCCA GACTTAGCTGCGATC	p000666	D	--
<u>24</u>	IM000642	GATCGCTGCTTCTGTAAATCCGCAACGA CAATTGTTATCTTCTCCTTTTCTTTCTTT ATTTGTTTTATTCTATTTTATTTTCAGAT GAACTCTCATGTAGCCCAGGCTGGTCTC AAACTCCCTCTGTAGCTGACGGCAACCT TGAAC	p000668	R	--
<u>25</u>	IM000643	TTCCTACACCATAGCATTTAGTTGTAGGC AGAAGCGATC	p000669	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>26</u>	IM000644	GATCGGCTCAAGGGCTCTAATTTAGTCT AGGAAGTCCTTAGGAAACATGAAAATCT CCGAGATAAGACCCGGGGTAAAAAGCTT GAGCCACGGAGTTAGACATGCCCAGGG TGGAGTCATGTTCAAGAGGTTCAAGACCC GAATCAGCTACGTAAATAAAGCATTGAG GCCTACCTGGGCTACAAGAGAGTATCTT TAAATAAATAAGATGATTTAAAAAAACT GTTTTCCCCTTAGATGGATTAAAAAACA AGACAAAACAAAACAAAACAAAACCCG TCTTCCTTCTTAA	p000672	D	--
<u>27</u>	IM000645	CTGTCCGTGTGGGAAACGTTTAGCAAGT CCGAGCGTGTTGATC	p000673	K	<i>Nmyc</i>
<u>28</u>	IM000646	ATGCGTTCGTATGACAGTTCTCCAAATGA CTGTCCCAAAGTCCCAGATTCTGGAAA CAGTAAAGACTGCCTCAAAGTGTAGTCA CTAGTCTATTATCTTAATCATAGTAACCA TTTGGGTTTGACTTGAAAACCTGTGACA GGGAGATAAAATTTCTGCCACTGTAGGTG AAGCTTGGAAGGGCTAACCCAATGAATA TGCTCAGTCGATC	p000676	C	--
<u>29</u>	IM000647	AGATGAAGCTATCCCCAGTCCCTAAGCT GAGTTCTGCCTGAGACTATTTGAAACAG GGTACCCCTGGGTCCCAGTTCAGTTGAC AGGTAGTGACGCATGAGAACGCCATAC CTGGTGGCCGTGCCCGAGAGTGCTGTC CCTGACCTGCCACTGTGTTCTCCAGAGC AGCTTTCCAATCTGCCTGCTCCTGTCTC CCCTGCCTGTTGGCACCAGGCAGCCAG AATTCCATTTGTTTGTGCTTCGCGATA GGCTCTTGCCATGTAGTCCTTCCTGGCC TAGAACTTGATATGTAGACTTCCCCCTT GGATC	p000678	C	--
<u>30</u>	IM000648	CCGTGTCCGTGGGCATGTGCGTGTACA GACAGACATACATGCCCCCGCATGAGTG TGAACACCAGAGGTCAACCTCAGGTGTC CTTTTGATGTTATCTACCTGTTTTTTGAA GCAAGGTCTAGGATTGACCAATGAGCCC CAAGTAGGGATC	p000679	D	--
<u>31</u>	IM000649	GATCCATAGGCAGAGAAGGCAGTAATAG GACATTGGTCATTGTACCTCATTTGTGAG GGGTCACCTTGGAATGTGCTGAGACTA GGTTCTAGGAGAAGCTCGCCA	p000682	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>32</u>	IM000650	CTGGCACTGTGTGGCAGAAACAGTGAAC AGTGTAGCGGTGCAGAATGTGTGTGCTG TGGGTTTTAGCACCAGGGCTGCATGAGA CTGCAGACATGCTTATGACGCAGGAAGG CTCAGGACACAGCACACATGTGTGCTAA CATACATGTTTCACCTCAGACTCAGCTCC CATTTGACTTTTAATTAATTTTTGGCCATT CCACAACAGAACCTTTTCTTGCTCCCTTT TTTCAATCTTATGTATATATCTCCTACATT TAGTTACAGGACTGTGACCTACAGTTTAA AACTCGGGGATC	p000684	D	--
<u>33</u>	IM000651	GATCCCTCCCCTCCCTTCTTTTTCCCGC CAAGCGTCGGCGAAGCCCTGCCCTTCA GGAGGCAGGAGGGGAGCTGAGTGAGGC GAGTCGGACCCAGCAGCTGAGAGCAGC GCAGCCCAGGGGTCTCGGCCGCGCAG ACCCCGGAATAA	p000685	K	<i>Myc</i>
<u>34</u>	IM000652	CTACCACAGCCCCAGTGCTCTGGAGGG ACTCTAGTAGCCAGGGCTGGCAGCTTGG TTTGGGCCAGCATCTCACTATGTAGCCT AGTTGTCCTGGAATTTGCTATGTAAATGT GGCTACCCTCAAACCATAGAGAGCCTC CCACCTCTCCTGAGATTATAGGCACATG CTACCATGCCCTAAGTGGATC	p000686	D	--
<u>35</u>	IM000653	GGAGCAGGCCCTTCTGAATCAACTTGGC AGAGTGAAGGAGGCACTCTCCACACAAA CAGGAAAAGGGCAGTGGTGACTTTCTAG GCAGGGAAGTGGTTACATTTTGTATTT GAAGGTGAAGAGTCGTGACATTCTGGGA AATAGGCAAGATGGCCGTTTCCCCTCAG CTACAACCAGCCATGCAGACCTCCTTGC AGGGACCTGGCTATCTACACTGGAACCA GAAAGGCACGCCCTGCTTTAGCCTCAGG CAGAACGATAATAACAGCGTGCTAGCTC AGTAGTCTGTGTGCTGGAAGGGTTTATG AGGAGGAAGTCCGCAATTACATTTTCT GGGCAAACATTAACCAAGATTGAAACCT AGATTTGAAGAGAAGTAGCAGGCTGGGA TC	p000687	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>36</u>	IM000654	AGATGAACCTATAAATGCATCTGCAGTCC TCAAATAAAGATGAATAGTAACCCAGAG GCGTGGTAGTGCGCTCTTCAAACCCAGT GCTCAGAAGGTGCAAACAAAAGGACCG GGAGTCCAAGGCTAGCCTTGACTAGAAG GGGCCATGTCTCAAAGAACAACAACCAA GAGCTGCTTATGGAGGTCAGTCTGTGTT CCCAGGGGGACAGCATCAGTCTAAGTTG GCGGTTGTTGTTGGCTGAGCATGCACAA ATCCCTAACAGCACATAAAGCAAGTTGT GTCACACACTCACAGTGCCAGATTAC TGGATC	p000688	B	Mm.1313 36
<u>37</u>	IM000655	GTCCATTGTGTAAGTGTGAGAGAGGAGTTAG GTTTAGAAAGCCTTCCTCAGATGTCCCT CAAAGAAGCTGCTACAACTGCCCTCATC CCACGTTGCCAAGGATC	p000689	D	--
<u>38</u>	IM000656	AGCTGTAGGGAAGCCCAAAGCACAGAC GACTGCTGCTGCTGCTGCGGTTCCCACT CTGGGTTGACCTTAGAAACGGGGGTTCA TCTCCTCCAGCAGCTCCGGAAGGAAG GTGAAGGGGACTAACCATGATGAGCTTT GCACACTGGAAGTCAAGGCTGAGAAGG GGCTGGAGGGAGGCAGGGAAGACATCC CTCACGGTAGTGTTACACAGCTGGCGTT GCGGGCTGCCAGGGTACTCATTGAGTC CATGCTGAGTCTCTCGGTGCCTCCTGAG ATC	p000694	K	<i>Gfi1</i>
<u>39</u>	IM000657	GATCGCCCCAGTTACCTCAAATTGTGTG AGTGTGTGTGTGTGTGTATGCATATAT GCATACAAGCATATACATGCATGCATATA TATAATACACATAGACATATATACACACA TATAGACGCATACATGCATTTGTATGCAT GCATCTATGTATGTACATATCCACAACCA AATATACCAAACACGCAGACACAGCACA CATAGGACAATAGTAATTGTGAATCTAAC TGGTGGGGTTTATGGGTCAAGAGCCAG GGTAGAGGAACTGGCTAAGGCTCTAAC CATCCTAGAGCAGGCACATCTACCAGGA AAAGAAACAAGGAAAAGAGCAGAGTTGA GGGTTACTTAACATG	p000695	D	--
<u>40</u>	IM000658	ACAGAATCTGTGGGTCATTATTACGTTTA TAGGAACAGGATTTTCTTCTTTCTGAC TCTACCTTCTAGAAAGGCCGACTTTTAAA TCCTCATGCTCTTGTCTATTGACAGGAAA AGATGGGCTTCCCACTGATC	p000700	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>41</u>	IM000659	GATCAGGCTGGCCTTGAAGTACACAGAGA CCCACCTGCCTCTGCCTCCTGCATGCTG GGATTAAAGGTGTGTGCCACCACTGCCC AGCTCACAAAGTAGTAGTAGGACTAGTA CTAGTACTAATAATAACAAACATTACAAC AATCTTAATTATTTTTGTTTCTACCTTTAA AATCTCCCAACTGTCTTTTATATTGCCT CAAGTCTTCCCTCAGTCCCTGGCCTTCA TAGCTTGACTTTTTTGCTAGAGGTTATCA GTGGCTCATCTCTCCTGAGATTGAGC TGGCTAAGACCACTATTCAGAGGGAGAA TGTAATGTCTCAGACATCATAGCCAGTC CTCAGTTCTCCTTTTGCTGACTGACCACT TTGCCAACTAGTTTTCTAAGCCATACC TTTTCTTTTAAAAAATAGTCTTTCTTATA GTGGGTGCTGGCTTTGAAGTTCTGTCCT CTTGCCTCACCTTGCACTGGTAGTAGAG GCTTGCAATTTACCG	p000702	C	--
<u>42</u>	IM000660	GATCAAGAACGAAACCCCTGAAAACATA AAACAGTAAGATAACAATAGCGTGCCTG ATTTTGTCCAAACCTTCTTGTCACCTGTC ACTGAGATTGTCAACTCCTTTTACCACC CTACATACGTTAGTTAGCTCAGTTTACGA GAGTTTGCAAAGGCCCCCACCAGTACCC TGCAACTTTACCCACCCCTGCATGGGAC TGTGAGAAAATGGGACTGGAGAGTAACC CTCTTCAGGCTCACAACTGAGCTAGTC AGAGCATCTCACGGGTCCCGGGACTTTC AGTGTGCTTTCCTCTTGGGTATTGGACTT TAAACAATGTGTACCGATATGGGTGAATA ATACAACATCCATGGAGAAATAAGCCAA ATCAAGACACTTCTTCAGAGG	p000703	D	--
<u>43</u>	IM000661	GATCAAAAACATCAACGTAAGGAGCCCT TAATGACGCTTTGTGACGGTTTAGAATG GTCTACCCAAACCTAGCCAAGTCTAACT ATGTTATGGAGGTGGTAAAAGCAGTTAA CCTAAACATCTGGGACACTCACAGAATG ATAGGTAGGTAGGTAGATAGATAGATAG ATAGATAGATAGATAGATAGACAGACAG ACAGACAGATGTTGAATAAAAAAGTGACG TTTACAGTGATGTTAGCTCAAGGCAGGG CTTTTCAGGCCATTTCCCCTGGTCTCAC CC	p000704	D	--
<u>44</u>	IM000662	CTACTAAGTCCAGAGCAGAGAAGGAGGC GCCGCCTGTGTGCACAGCGAGTCTGG GAGAGACCACCGGCCCAAACCAAGTAAAC ACAGGGCACCCACCGTGCTCCGATC	p000706	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>45</u>	IM000663	ACAGTAATCTGATTATCTTGCAGTAGATA ATTTGTCTACCTGTTAATGACTCTGCTTC TTGAACTACGTCCCAGTAGATGCCATGC TTTCAGCCTGGTAAGTGACACTAATACTA CCTCCAAACTGTCACTTGGATTGTCAGG GTTTTGGTGTGGTGATGATACAGGAGAA ATGTAAACACGGAGTTGATGATAGAAA GGAGTCACTAATACATTTTCTTAGGAAAA GTCAAGTGACACACAGCAGAATCTAGCT GAAGGAGCTCCGCCAATAGGGCTGGAA GATAACTCTCGCACTAACCTGCTTTATTA GGAAGTGTAGGAAAGGCAGGTCTGCAG CACAGTTGAAGTTTAGGTTGCTGAGAAA GTTTCTGCTCATATTTATTCACCAGTGAT GATC	p000708	D	--
<u>46</u>	IM000664	GTTTAGCAAGTCCGAGCGTGTTGATC	p000709	K	<i>Nmyc</i>
<u>47</u>	IM000665	AGGCAAACCCATGTGAGGCCTTCTCACA TCTTTCCTTGGATGCCTGCACACACCTG ACTTGACAGACTTCAAATCAGACTTATCA ACTCACCTCTTCAGTCCTGGGCCTCTTC CTGTATTTCAATCTTAGATAGAAAATTGG TTCCACTGTCTACCAGCCTGAACCAGG AATGCAGAGCCAACCACCCCTGGGGTGT CCCAGGCAGCTGGGCTGGATGCTACCT GTCATGCTCTTGATC	p000710	C	--
<u>48</u>	IM000666	ATGTATGAGTGTGGGGCTGGGTTTGAAC CTGTGTCACCTTAGGACTCTCTGAACCT CGGTTTCCTATTAGACGGAGGGGCTATT CGGAGTCCTCATCTAATGGAGACACTTT GTGGGTATCAGAGGGCAACACTGTGGTA TTGGGGGTGGGGGGTTGCTGCTTAGAG CTCAGAGAAGAGGAGTTTGGCTTGCTCT ACAGAACATGCAGGCTGAGGTGTGGGT GCAGGGTTTCCCTGAGGCCCGGCTCT GACCCTCTCCCCACTCCATTTCTGCGC AGGTGAGCGACAAACGTTCCAACAGCTT CCGCCAGGCCATCCTTCAGGGAAACCG CAGGCTGAGCAGCAAGGCCCTGCTGGA GGAGAAGGGGCTGAGCCTCTCTCAGCG GCTCATCCGCCACGTGGCCTACGAGACT CTGCCCCGGGAGATTGACCGCAAGTGG TACTATGACAGCTACACCTGCTGCCTCC GCCCCGTTTCATGATC	p000711	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>49</u>	IM000667	GATCATTTTTCTCTCGAGATGGATTAAG CTATGCTGCAGAAGGACCCGTGTGTGTC CTGTGTGTGTGTGTCCTCGCCGGCGAGA CTCCTTATCACACATGACAGCTTCAAAGC CCCCAGATTCAATAGGTTCCAGGAGTTC ACATTTAACTCATGGGGTCAAAGTGC AGGCAGATGGTGGAGCCTGTGGAAGGT CATCAGACAAACAACCTGGTGGTTGCAG CAGAAATCACCAGGCAAGTAG	p000712	R	--
<u>50</u>	IM000668	GATCTGGCTAGCAGGGAGCCATTTACAG CTCAGACATCTATCATCCTTA	p000713	D	--
<u>51</u>	IM000669	GATCATTGTACCTCACCTGTCAGTTTGAC AGGTGGGAGGTGATATCTTTTCATTCA TGTATTCTTTGAAAGTTTGTTTCATGCATA TAATACATTCTGGTTCAATTCACCACTCC ACCCTTTTGTATCCCCTGCGTACCGAGC CCCCATTTTCTACCAAGTCTTACTGTTA TCTCAGTTTTGGGGCTTAGTTTTTGT GTCTTGTTTTGTTGTTTTGAAACAGGGT CCCGTTATGCAGCCCTGGCCCTGAACTT GCTAAATAAACAGGTTGGCTTTGAATTC AGAGTTCTGCACACCTCTGTTACCCAAG TGCTCAGATTAAAGGCGTATACTACCAC	p000714	C	--
<u>52</u>	IM000670	GATCAATTCAATCTATTGCAATAACCTGG TTTTTTTTTCCGCAACTCCAAGATGGGG GGGGGGGGGCCAGTCAGGAGAGGTTT CAACACAAACGCACTAGTATTACACACA GAATCTCCTCCACTGTTCTTCTTTGC TTTAAAAGTCTTTGTTCCGGAATCTATAG ATAGGGAGACAGATGGCTAGCTCCCCAA GGCTGAGAGCAGAGGAGAGTATAAACA GGGAAGTCAAGGGGTCTGGGAGGGCAA GGTAAGGAAGCCACAG	p000715	D	--
<u>53</u>	IM000671	CAATGCCTTCCCCGCGAGATGGAGTGG CTGTTTATCCCTAAGTGGCTCTCCAAGTA TACGTGGCAGTGAGTTGCCGAGCAATTT TAATAAAATCCAGACATCGTTTTCTG CATAGACCTCATCTGCGGTTGATC	p000716	K	<i>Myc</i>
<u>54</u>	IM000672	TAGTATTCAGGAAAAAGGAACTGGGAA ATTAATGTATAAATTAATCAGCTTTTAA TTAGCTTAACACACACATACGAAGGCAA AAATGTAACGTTACTTTGATC	p000718	K	<i>Myc</i>
<u>55</u>	IM000673	GATCAGAAAAACAGCCCATTATTCAAGAT TCAGGT	p000719	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>56</u>	IM000674	TAACTTCAATTTAATAATTATCACATGCTA GGAAGTAAAGAGGTGCACAAAACAAACC AACAGTGGTTCTATCCTGTCTAACAGAA GAAACTACAATTGTGGTTTGGGATGCCA CATAAATGACAGCAACGGGACCTACAGA AAATTAAGTCACAGAGAGAATGGACCAT TTCTGCAGAGACCTGGAAAACAGACAAG GGAAGAAACATGGTGTGTCTAAGTGATG GGGCAGGTGGTGCAAACGCTAGAGGCA AGCAGAGGGGATATGAAACTGTGCTGCA CAGCTGGACAGAAGGGAGGCTGGAAGG GAAGAGAGGACCCTCTGTTTTGACTCAA TGGCTAGATGCCATGTGCCAAATAAGAA AGCACTTGGGGGGTTCTGTGGGAAATCG GAACAGAGGGACTGGAATCAAACCTCAA CGTTCCTTGCACTCCAGATAAGAACC AGGCTTTGAGCCAGGGCCTGGGAAGAG GGCTGGCCTACATATCTCATTTTAGAGAT GAGCAAACAGGACTGGGAGCTCTAGGT CTTCAAGTGACACGCTTGCTTGGCCCGCA GGAGACCCTGGGTTTGATC	p000720	D	--
<u>57</u>	IM000675	GATCATGTGTCATGGGTCAACAGAAATAATT CTGAAAGGCTAAGTCATTTCTTCTACCCC CAAGAAAAATCAAGAACCCCCACATTA CAAACCTTCCGTAGTAACTGAGAATGG AGCCATGGCCAGAGCCCCTCTGCTCTCC CATCCCCCAACCAAGAACCAAAC	p000721	D	--
<u>58</u>	IM000676	ATATAACTTCTTTTTTTTTAAAAAAGAATT ATTTATTTTATGTATATAAGTTCCTTATAG CTGTATTGAGAGACGCCAGAAGAGAGCA TCTGATC	p000722	R	--
<u>59</u>	IM000677	GATCATAGCACACTGGGGTGCCATCTGT CACCCCTAGACAAACATCTTTAACCNGC ATCTCTTCCTGAAGCCCACTTGGACCAC CCTTTGAAAACCATCACCAAGGCCAGT AAGGTACCCGTGGTGACTCACCTCAGCC TAGCCCACCATAGACGCTTAGCAGAGCA GGTGTGTGTAAGTCAGAGCCAGACAATC AGAACACTCTCCCTGCTCCAAAGTAGCA ATGTAAAAAATTGAACCCAAAGTTG	p000724	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>60</u>	IM000678	GATCAAAGTAACGTTACATTTTTGCCTTC GTATGTGTGTGCTAAGCTAATTAAGCT GATTTTAATTTATACATTAATTTCCAGTT TCCTTTTTCCTGAATACTACGCTGTGCAT TCTGTACAATCCCCAAACGTATACATACA CACTTTATATATACACGATAATCTAGCTT ATTAACCAACCAGAAACATGAGTCTTTTG CTCTGTGCATTGGTTCTAGATTTATTATA TAATGCATATTCCTCGGGATTGCTTAT CC	p000727	K	<i>Myc</i>
<u>61</u>	IM000679	GATCATTTGATGCTTCAGATAAATATGTA AATGGTGAC	p000728	B	<i>Mm.1278</i> 81
<u>62</u>	IM000680	GATCAAGATAATCCCCACAGGCATGCC CAGAGGCCCATTTCTAGGTGAGACTAT AGTCTGTCAAGTTGACAATGCTAACCATT GCAGTGAGGGAGAGAAAGAAGGCCAGG ATGGTGCCTCTCTGTTACTCTGCTTACCC ACGGGGTGCAAGGACAGTGGGGGATGG GCCTGAGCTTCCTCATGAACACACACAT GAGAGCAGTCAGCACATGGCCTCTTCCT CTAAGCTTCACAGTGGCAGCCGCACCTC TGCTGTTAAGACCTAACATGTGGCCGGG CAGTGGTGGCACACGCCTTTAATCCAG CACTCGGGAGGCAGAGGCAGGTGGATT TCTGAGTTCGAGGCCAGCCTGGTCTCCA GAGTGAGTTCCAGGACAGCCAGGGCTA CACAGAGAAACCCTGTCTTGAAAAACCA AAACCAAAACCAACCAACCAACCAACCA AACAAACCATCTAACATGTACATCCTATC CATGTGCACGAATCATAC	p000729	R	--
<u>63</u>	IM000681	AGACCAAGTGCCGGAGCCGTTCTGGCT GAGGCAGCCCAAGTCCTTGAAGAGCTTG AAGAGGTCGCTGCGGAATTGACGCCG ATGAAGGCATACAAGAAAGGGTTGACGC AGCAGCGGACGGAGGCCAGGCTGTAGG TGACGTCATAGGCAATGTTGAGCTGCTT GCTGGTTTCGACAGCTGCTATTGGTGATG TTGAAGTTGGCCACCGTCTGAGCCAGGA CCACCCCATTTGAGGGCAGCTGGAAGAC TATGAAGACTACCACCACGGCAATGATC	p000730	A	<i>Cmkbr7</i>
<u>64</u>	IM000682	CCCTCTCAAGCCTTCCTTGTTACTTAGCC TCTATAGGTCTGTGCATTATACCATCATT CTTTTAATTTACAGCTAATATCCATTTATA TATGATTATGTACCATATTTGCCTTTTGG GGTCTGGATTGCCCTACTCAGGATGACC TTTTCTAGTTTGATC	p000731	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>65</u>	IM000683	GATCATGATGTTTGTTGAAGCAACAGAAA CTATAAGACAGTGCCCAAGAGCCTCTCT GGAGATAGCC	p000732	D	--
<u>66</u>	IM000684	GATCGTGTTAGACACAAGTAAGAAATGA ATGAGTCTTCCTGATTTTTTAAATTAACCTT CTCCCCATATTGGCTGTCACTACTTTTTA AATCAGAAAGGAGAATCTGGACGGTTCC AGGCCTGCAGCGCCATGCTTGCAAAAG GTTTACAGAATCGCTCTGGACAACT	p000734	D	--
<u>67</u>	IM000685	CTACCACAGCATCTTTTGAGTGTATATAG TCAGTGTGCTACATGTTATCTATGAACAT ATGCAAATGAGGTTTGAGAATTAAAGTTG CTGATAGACTCATGGGTTAGGGGTTTGA TTGCCTGCTAATGATC	p000735	D	--
<u>68</u>	IM000686	GATCACGAAACGGTTGACTAAAGCAAGA CTGAACCACAGGCAGATACCAAACCCAA AGCTCTATGTCTAGTGTCTAGAATACATA GGTTTGGGTAGCCATGCCCTGTGACCC TGCCACCTGCAGCACACATAAGACAATA CTATAGACAACCACTTCTGAGTCAGAATT GCAATGATGTCTTTGGCAAACACTACTCTAG TCTCCTTTGGCCAGGAGCTGCTAAGTGG TTCAGGCTGAGGTACAATCAACCTAGGT AGGTGGGACTGTGTGCCCTGTGCTCCT GGGTGGCCTTCATGTCTGCTATGCTTGC CCTTT	p000736	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>69</u>	IM000687	GATCATGTCAACTATACCTGGACACGGA CCTTCATCCTTGCTGGTTTCACTACCTCT GGCACCCCTGCAACATCTTGCAGTTTTTG GAACCCTGTGCATCTATCTCCTCACACT GGCAGGGAACCTGTTCATCATTGTCTTG GTCCAGGCAGATTCAGGGCTGTCCACTC CCATGTACTTCTTTATCAGTGTCTCTCC TTCCTGGAACCTCTGGTATGTCAGCACCA CAGTGCCACCTTGCTGCATACCTTGCT CCATGGGCCTTCACCCATCCCCTCGTCT GCATGCTTTGTCCAGCTGTATGTCTTCCA CTCCTTGGGCATGACCGAGTGCTACCTG CTAGGTGTCATGGCTCTGGACCGCTACC TTGCTATCTGTCGTCCACTGCACTACCAT GCACTCATGAGCAGACAGGTACAGAAAC AGTTAGTTGGGGTTACATGGTTGGCTGG TTTTTCAGCTGCCTGGTGCCTGCAGGTC TCACTGCCTCTTTACCTTATTGTTGAAA GAAGTGGCCCATTA	p000737	C	--
<u>70</u>	IM000688	CTGTCAATTCATCCAGCTCTAGGCCGCT GTCTGGCTCGATGCTTATTGGTTTAAAC GTGCCGATGCATAGGATTCTACAGTCAG AGTGGCCTAAGCAACAGCTAAATATTGTT TTCTTGCTGTTCTGGGAACTAGATGTTCA AGGTCAAGGCGTCAGTAGCTCTGTTATG AGACCTCTCTGCTGTCGGGCTGTGTCTT CAAGTTTTTCCCCCTCTGTGCATGTGT GTTCTATTTCCTCTGCATGAAAGACCAG TAGAGCCAAGTGGTGGCACACACCTTTG ATC	p000738	D	--
<u>71</u>	IM000689	GATCATGAGAGGCGAGAAACCCAGACAT CTCTAACTCTTCTTGCCAACTCAGGAGC CACCTGTGGCCCCAGCTGGCCACCAGC CGTTCCTCCCTCAGAGGCCTCCATTTCC ACAAAAGGCCTTCCTGGTTGTTCAGGAC AGAGCCTGGTTTCCCTGATACCCCTTCT CTCAGTGGCCACTGAAGTTACAGGGATG CAGCCAGCCGTGGTTGCCATGTCTGTAT ATGCTAATCTCGAATTCCA	p000739	D	--
<u>72</u>	IM000690	GTTTGTCCGCATGAGTCCCAGGGACCAC TCAGAGTGGCTGGCAGGCATTGTGGAGT GGAATGTGGGAAGACACATTCCCAGCCT TGTTTGAGCTTGGGACTGTCTGTGTTTT GGGATGATC	p000740	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>73</u>	IM000691	GATCACCTGGGAAGGGGGAAAAGGACA AGTCTGAGCTCCCAGCCCACATTCTCCT AGGGTAGCAGCTCCCTCACTTAGTGT	p000741	D	--
<u>74</u>	IM000692	GATCAGTTCTTATTAACAATACAGACTT AGGCAAAATGAGTCAGAAATAAGGATAT CGCATATCCCGAGACCATTGAACTCTA AGAAGTATTTTCTATTATTAAGTAGTTCA CCAGGCAGTGGTGGCACACACCTTTAAT CCCAGCACTCGGGAGGCAGAGGCAGGT GGATTTCTCAGTTTGAGGCCAGCCTGGT CTACAGAGTGAGTTCAGGACAGCCAGG GCTACACAGAGAAAACCCTGTCTGGACAA ACCAAAAAAAAAAAAAAAAAAAAAAG	p000744	R	--
<u>75</u>	IM000693	GATCATCACAGATGACATAGAACCAAAC TGTAACTTTCTAGACTACATGTAGCAGAC ATTT	p000745	D	--
<u>76</u>	IM000694	GATCATACATGAATACAAGCAGGCTTCT GGTATACTCTTAAGTTGAATTCTGTTTTCT TGTAGTCGTAGTCTTGTCTTTTCCAGTTT TAAATTCTAGAACAGGTATACTGTAGAGC ACCCGCCTCCCCTTGCTCTGGAGGTAGG GTAGAGTGGGAGTTAAGGTCAGTTCC	p000746	B	AA65702 8
<u>77</u>	IM000695	ATTTCTCTTGTAAACTCACTTTCTGTTCA CCCATTTTGTCTGTGTCCTTACTAAATTA TTTCTATATAGGAATCTTTGTATCTTCTGA TATAAGCTAGCGCATGGGTACCACCAGC ACCCAAGTCATCTGCTGAGGTGCTTCTA ACCTTGCTTGATTCAGTGTCTTCAACAGA AGGTGGAGTAAACAGGTCATTTTTTACC CTAGAGAGTTCAGATC	p000748	D	--
<u>78</u>	IM000696	GATCTCCGGGTGCCAGACTTGCCCAGCA AGCACTCTTACCTGCTGAGCCATCCTGA GGGCCTGGATTTAAAAAAAAAAAAATATTG ACATATTGTTT	p000749	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>79</u>	IM000697	GATCTCCTAAAACCTCCCTGTGTCAGGAA ACTTTCTGTGCTTTTGTATTGCGTTCCTG TGTTCTGGAAGGCCCCACGCCTTCAT CCTTGCTAATTCTTTTGGATAGCTTGTT GCTTTAACTAGATTGGCCCTTTCTTGGCT AGTATTTTCTGCTGTACCTATGAGTGGTG TGGGAGAACTGTGCAGACTTCCAGGAAG CGCAGCCATGAAGCTACATGTGCCTATG TGTAGACACATCATGGATTTTCTTACTAG TTTACTAGTGGGTGATAATCTGTCCTTTT GAGCTCTCCAGAACGTTCTAGAAGCTTA AGGAGAGAAAACACTTAAGAGAG	p000752	D	--
<u>80</u>	IM000698	ATCTGATAGTAAGTAAAAGGACAGCTAAA GATGAAGGGAAAGCAGGAGAGTCCTGG AAGAAGAACTAGTGTTTCTAAGAGTTCA TCATTGATAAAATGCAAAAGAAGTCAATT ACATACATGTTTAGGAACTGAATCCTCT TGTTTTGGGGGATGTTTGTTTGAGGCA AAGGCTCTCTTACAGAGCCCTGGCTGTT CTGGAGTTCTGTATATCAGGCTCTGGCC TCAAACCTCAAGAGATC	p000753	D	--
<u>81</u>	IM000699	ACATCAAGAGGAAGTTGGAAATGTCATC TTTAGCTATCTTATATCCTGGTAGCTTTA AGATTTCTTTGTGTGACTTTATAGTTCT CAAAATATTTTAAAGGGTCAGGGGAGGA AGCACTTTCAAGAAATGAGATGGGAGAG GGAATGTCTTTGTGTTGGCCTGGAGATC	p000755	D	--
<u>82</u>	IM000700	AGCTATACCTGAAATTTGGCCAAGAACA GAAGCTCAGGAAATAGTGTGATTTAAAAA CCAAAACCAATTTACAAAAGGAAGACTGT GGTGTAGATC	p000756	D	--
<u>83</u>	IM000701	CCACAACCTGAAAGCAACACACACAGTAT TTTTCTGTGGGTTTTAGGATGTATCCACA CTCCCGAACTTCCTTTCCCTGAAGCACC CCTCAGTTTACTCTGAAGCATGGTTTGA GTCCAAGGCCAGTGTCAACTTTCTGCC AAGTCTCAATGGCAAAAGTCTGTTTAAAT CTGCTCAGGCTAATGTAGATC	p000757	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>84</u>	IM000702	CTTCCAGTCTTTTTAGCTATTTATTGATAT GAATTCCTGCCTTATGTATCATCCAAGA TTCTACCTAAAATACTTCCAATAAGTATC AAGGACCACTCAAATATTCACACTATTGGAC TTAGAAGCTCCACTCTTAAAAATAGATTCT TATAGAAAGAGCCTGAAATGGGGGCATG AAATGGGTCCATCTCCACCATCACGCAC ACATGAACAAAGAAAAGGAGGAAATGGT GTTAAGAAAACCTTACATCATACTATTTAA AAATAAGGAGGAAGGAGGGAGGGAGAG AAAGAGAGAAAGCTCAATGCTTAGGCAA GAGTGCTTAAGAAAATTACAGTTAACAGA TC	p000758	D	--
<u>85</u>	IM000703	GATCTCCTAAACTCCCTGTGTCAGGAA ACTTTCTGTGCTTTTGTATTGCGTTCCTG TGTTCTGGAAGGCCCCCACGCCTTCAT CCTTGCTAATTCTTTTGGATAGCTTGTT GCTTTAACTAGATTGGCCCTTCTTGGCT AGTATTTTCTGCTGTACCTATGAGTGGTG TGGGAGAACTGTGCAGACTTCCAGGAAG CGCAGCCATGAAGCTACATGTGCCTATG T	p000759	D	--
<u>86</u>	IM000704	GATCTGAGTGCTGGGAACCAAACCTGGG TCCTCTGCAACAGTTTGTGCTCTTAGCTG CCGAGCTTT	p000760	R	--
<u>87</u>	IM000705	GTACGGCGATGGGCACAGGCTTCGGGA CAGTCCGCGCGACGCTCAGGCGGACAA CGGGAGGCGGGCGGGGAAGGCAGGGG CTGCAGTGTCAAGTCCCTGACCCGGGA GGCTCGGAAACTTCACTGCCTCTGCGCA TCCGGCATGGCCCCTCCCACTCGGACTT CGTCAAAAAACCGCCACCGTGGAGTGTC CCAGTATGTGCGGTGTGGGACAACTAT CGCACTGTTGCCCTGGCTCTTCTCCTAG ACCCCTTTGTGAGCCAAAAGAGAAACG CTGGGCAGATC	p000761	B	Mm.2739 3
<u>88</u>	IM000706	GATCTCGTTACGGATGGTTGTGAGCCAC CATGTGGTTGCTGGGATAA	p000762	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>89</u>	IM000707	CTGGGTTGACCTTAGAAACGGGAGTTCA TCTCCTCCAGCAGCTCCGGGAAGGAAG GTGAAGGGGACTAACCATGATGAGCTTT GCACACTGGA CT CAGGGCCTGAGAAGG GGCTGGAGGGAGGCAGGGAAGACATCC CTCACGGTAGTGTTACACAGCTGGTGTT GCGGGCTGCCAGGGTACTCATTTGAGTC CATGCTGAGTCTCTCGGTGCCTCCTGAG ATC	p000763	K	<i>Gfi1</i>
<u>90</u>	IM000708	GATCTCAGGAGGCACCGAGAGACTCAG CATGGACTCAAATGAGTACCCTGGCAGC CCGCAACACCAGCTGCGTAACACTACCG TGAGGGATGTCTTCCCTGCCTCCCTCCA GCCCCTTCTCAGGCCCTGAGTCCAGTGT GCAAAGCTCATCATGGTTAGTCCCCTTC ACCTTCCTTCCCGAGCTGCTGGAGGAG ATGAACTCCCGTTTCTAAGGTCAACCCA GAGTGGGAACCGCAGCAGCAGCAGCAG TCGTCTGTGCTTTGGGCTCCCTA	p000764	K	<i>Gfi1</i>
<u>91</u>	IM000709	GGAAGAAGTGTGTGCAGGCCATGGTCAA GTCCTGCATGGCTCCCATCTGGGTCCAG CAGCACCAGCCTCCAGTGCTTGCTCCT GATGTCCCAGTGA ACTCAGGTCCTGAGC AGCAAATCCCAGGGGCCAGTCCTAGGG AGAAAAAGAACACACTGCCATCTCAGTG CCTCAACAGAAGCAAACCTAGGCGTCAG GTCATGTCCTTGTTACCCACATCACACCT AGACTTCCCTGGGTATCATGCTCTGTGT GAGATC	p000765	B	Mm.1535 12
<u>92</u>	IM000710	GATCTAAGGATATATCATTCTAGGAGAA AATGAATATTTATGACCTTGATTTGTCA ATGTTTTTTTAAATATGGCATTAAAGCCAC AGAGATAAAAATAAGAAATAGATACATC GAATTCAGTAAATGAGGAAGTTCTTGT GATTCAACAGAAAC	p000766	A	<i>Mtm1</i>
<u>93</u>	IM000711	GAGGTAAGTCTGTT CAGTGTAGCTATCC TTAGCAGCTAACAGTCCTCAAACTTTTT AGAGATC	p000767	D	--
<u>94</u>	IM000712	CTACAGATGCATTATTAATATTACTTTTTA AAAAAACCCAGTATACTGCTTGAAAAACAG TGAATGCAATGGGTTCTCATTACCTTCC TGCTCTCAATCAATCTCCATCTCTAAAGC AAGAAGTGGGGGCCCTTCTGGCTGAGC GAGGGGTGAAGGGAGGGGAAGAGATC	p000768	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>95</u>	IM000713	GATCTGGAGAAGATGTCAAGTTTTAAAT GAGGCAG	p000769	D	--
<u>96</u>	IM000714	GAGTGAAGCAAGAATTTGGAGCCCAGCT GCCGCAGCCTTTTTCTTTCAGCAAAGC TCGGGAGTGATAGATATGCATGAACCAA AGCAAAGCCTTGAGAGTGCCACTTGGCC CTGCCTCCTGAGGGTCTCAGGGCATCAG CTGGAGACCACCCTGTGACCCACACATC ACCGACTATGAAAACAGCTCATCAGAGT AATAAAGATC	p000770	D	--
<u>97</u>	IM000715	CAATGAACAGGACACATGCTTCACACGA CAGTCCAAAAATGCAAAGTGGAAGAA TTCCACAGCCATAGCCTTCATTACTAGAT C	p000771	D	--
<u>98</u>	IM000716	ATGCCTTCCTGGTAGAAGAGGGCCATGC TGTGGCGGGGAGGGGCCACTCAATTTTT CCTGCTCCCTTTCCCTGTCCCATATTCTC AGGAGCTTCTAGAAGCGTAGCCTGCATC TCATGCCCTGACTTGGCACCAAATGCTT GCTTTGTATCAACACCGCTTTCTCTTCTG CTCTTTCCAGCTCGCAGCCATTCAAATAA TACCACCCGGTACCCGTGGAATCAGGAG CAGAGATTCCAAATTGAGTCCTAAATCA AATCCAAATGGGCCCGTCAGCTAGATC	p000773	D	--
<u>99</u>	IM000717	AGGCGAGCGGATTACTAAGGACTGAAAG ACTCCTAAGACTTGTCTCCTGCTCCCTG GCCAGCGGTGGAGCTCAAGCAGAATTG CAAGCTCAGCTCAGGTCTCAGTGATGCA AAGCACCCCTCGTTACTCCAATGTGTGTTA CTCCTACAGGTGGGCTGCCTTCCACTTT CAAACACCCGCACAAACAGACCTCCAC CGTATGCCAGAGCATCTGTTGATGCTT TCTGGAAACTATGCAAGCCCAAATTTAAT ATCCAATCAGATC	p000774	D	--
<u>100</u>	IM000718	GTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTTACAAGGTCTCATACAGAATCC AGGCTGGTCTCAAACACTGGAGTCAAG CCATCTTCTACCTGGCTTAGCTGGGGT CACAGACTTGTGCCATCATGCCCAATGG AATGCTGTTCTTTTGGAAAGCCTGCTAC TGTCATATACTGTCATAGGAGTTAGCGA CTGCTGGCTTATTCCTTCGCTTTGCTTGG AGATC	p000776	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>101</u>	IM000719	CCCCCTTCCTGTACCTCCTGACCCCTT GCGCAAAGGAGGCTCGTGCCCGCTGT CCCACTGGGGGATGGGGCTGGGGTTGA GAAGGCTAGTGAGCGCCTCTAACGCTCA GGAAGTGAAGTTTGTGGTTTGGGGGCT GAGCTCCGAAGGAGATTAAAAAAAAAA AAAAAAGTCAGAGAGACAGATC	p000777	D	--
<u>102</u>	IM000720	CTTTGTATAAGCAGCAAACAAAAAGCCA GAGGCAGTCCACAGATC	p000778	D	--
<u>103</u>	IM000721	ATACAACAGGAGCAAAGCTGGAGGGGA ACAGATATAGAGGACAGTTCAGGGCATC TGCAGAGGTGCTGTGGAATGGGGAGGG GACAGTGGATAAGGGGACTTACCCTGAG CATCTCGGTAATAAGCATGGGTCACACT GCGGAAGCGCTCCTGTCTGCAGTGT CCAGATC	p000780	A	<i>Rab37</i>
<u>104</u>	IM000722	GATCTATGTCATCTTCCAGGACTCAGAG TTAAGAGAGTTACCAAGTGAGAGCTCTC ATCACCTTCTGAAGCAGTTGAGAATTGG AACCCAGAAAGATGCACATGCACGGGCA CACACACACCCACGGGCACACACCCAC CCACCCATGCAGAGAGAGAGAGAGAGA GAGAGAGAGAGAGAACTCACACTGGTAC TGCAGTAAACGGGAGCTTGTTT	p000781	D	--
<u>105</u>	IM000723	GATCTTCTTTCTCTGCTCAATTAGTTCAC TTCTGCTTTCATCTCCTTTTCTTTGATAA ACCATGAGTTTCATTAGGGCTATTACAAT CACATGCAGTTTTTCTTATAGTA	p000782	D	--
<u>106</u>	IM000724	GAATTAGGCCTAGAAACATTAGAATCCA GACCACGGAGCTCCCCAGATC	p000783	D	--
<u>107</u>	IM000725	GATCTTGTTCTAGAACGACCCTGAAGGC AGCAGAACAGAGCAGGACTGAAGGCCA CCAAGGGGATTTCAACTCTTCAGAAAAA ATAAGTGACTCACCTTCTCACAAAGAGC AAGAATCACAGAGGTCAGATTGTCTCCT CCTGCCCATCAGGGACAGAGTCCCCCAT CTTTGCCTTGCTCCATCTGGCAGGTAAG AGATGGGAAGTCTCCTTCCCTCGGTCT GCAGCATCCCTGGCATCCCTGGGGAGT GTTGGCACAGAACCCCCCTCCCAA	p000784	C	--
<u>108</u>	IM000726	GATCTGTGTGGGCAAAGCCCATGTGCTG CAGTGTGTCTGGGTAGAAATGAGTTGTG TGGTGCTCAAATGTAAATGAAGTCCCTG TGTT	p000785	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>109</u>	IM000727	GATCTCATTACAGATGGATGTGAGCCAC CATGTGGTTGCTGGGAATTGAACTCAGG ACCTTTGGAAGAGCAGTCAGTGCCCTTA ACTGCTGAGCCATCTCTCCAGCCCCCA CCTTTTTTTTTTAAAAGATTTATTTATAGT TTTTGCTTTTTTAACAGTACTGGAACATC TCAGTAATTGCTAAGTTGTCCTTGCTCCA GGTGAGCAGTCATATTTCTCCAATTCTG GTTTCCTTACTTGTGTCAGAGACCAAAT AGCTTGTTAATCAGTTAGAGCTCTTAG TTACCCATATCTGTGTAGTAA	p000787	R	--
<u>110</u>	IM000728	TAAGAACATAAAAGCAAAATTTGGAGGCT CAAGATTCAGTTTAGTTGCTAGAGGGCT CACATAGCATGCCCTCCCCACCCGGGAT TCCATTCTCATTTATCGAGGCATAAGGCC AGGTGTGGTGGGATATGTGCTGGGATG CATAAGATC	p000788	D	--
<u>111</u>	IM000729	GAAAGGCACACTGGTGAAGGCTGAGGA CCACCAAAGCTGCATTTCTGCTAGGCTA GGTAGAACAAAGAATGGTGCTCCACTAAG AACTCAAAAAGCCACAGCCCACCCCTGA GGCCCTCCATCTGACACATGCCGGTCAC CTGTCCTCCCACAGCCCAGCACAGAGAA GCCACCATCCCTCCCCTTCCCACCTCCT GCAGCTGACAGTGTGCATCTTTCCGCAC ATTCTCTCTCCTCAATCAGGTCAGAATG TATCCAAAGATC	p000789	D	--
<u>112</u>	IM000730	CACTGAAAATGGCTAGAATTCTGGTGAT GGGTGAGCCGATC	p000793	D	--
<u>113</u>	IM000731	GATCGGAGTCCCTCGTTTCAGAGGCCCC ACTTCTATGGCTCCTGCCTTCCTTGGCTA CATCCATTCTGCTGAGCTCCTGGAAAC CTGTGTATCAAGTCTTTTCCAGTTAGTGC GTTCTGAGTGGCTCTAGAAACCGCTTCC CATTACAGCGAAAGACCCGTATAAACCA TGTTCTCTTCTCTGTGACAAGAGACAAC AGACACCGCACAAAGGACTGTCTGGCCT GGGGGGGGGTCCCTGGTTCACAGCTTC AGTCCTGA	p000794	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>114</u>	IM000732	GATCGCTCAATATAACAGCAACATGCCA AGTGCCACTTGTAAAATTTGTTGTTGAGC AGTCTCATTATCAACTGAAGCACAAATGTC AGGCTAGCAAGAGGCAGGTTTCAGTTGTT GATTAGCGATAGCACACACAAGCCAGCA CATGCTTTTTCTGTGAGTTCTAT	p000795	D	--
<u>115</u>	IM000733	GATCGCTGAGTTTGTTTACAGAGCAGGG ACGCCTCAGCTCGGATGCCAAAGCTACC AAGAGCTGCAAACGCCAACTTAGCAGAA GCACACGTACTCCC	p000796	A	<i>Cited2</i>
<u>116</u>	IM000734	GATCGCACAGGTAAAATGGGGACTCACT TTAGCTAAAACAACAACAACAAACAGCCT GATGAGTCGAAAGTCTCTTTAGGTTGCC CTCTGTTCTCCAGCCCCACATCCTGAAG GCTGTGCATTCTCCACAGCAGTCTCA AAATAACCATAGTGCTCAAGTCCCCTGTA TCAAATGGTGGTATCTGCATCCACCCTA CAGGTGTTCTTTGATTCTTTCTTTCTTTG TAAGTGTGTCTGGGTGTTTGCCTGAGC GTATGTATGCGCCTAGTACCTGCAGAGG CCAGAATAAGGTGTCAG	p000797	D	--
<u>117</u>	IM000735	GATCGTGAGAGGCGAGAAACCCAGACAT CTCTAACCCCTTCTTGCCAACTCAGGAGC CACCTGTGGCCCCAGCTGGCCACCAGC CGTTCCTCCCTCAGAGGCCTCCATTTC ACAAAAGGCCTTCCTGGTTGTTTCAGGAC AGAGCCTGGTTTCCCTGATACCCCTTCT CTCAGTGGCCACTGAAGTTACAGGGATG CAGCCAGCCGTGGTTGCCATGTCTGTAT ATGCTAATCTCCGAATTCCACTTCCTGTT TAGATTCTCGG	p000798	D	--
<u>118</u>	IM000736	ACTGTCCGTGTGGGAAACGTTTAGCAAG TCCGAGCGTGTTTCGATC	p000799	K	<i>Nmyc</i>

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>119</u>	IM000737	ATTTCTTTTGTGAGTACTTCATATAAGAGC TTCGCATCTACACCACTCTTGCTCGCCA CTCCTCTTTTCTTCTTTCATTAATACTGT CCACTCTCCAACTTCATAATCTCTCTAA TTACTATTGTTATTTACACACACACACAC ACACACACACACACACACACACACACGT ATATGTAACCTACTGAATCTTACTAAATA GCTTTACTATCTTCCAAGTAACAGGCACT TGATAAATCTTCTGTCAATCTCCAGAAC AGAAGCCTTAAGAGTCATTTAAGTTCTTT TATCTCAGGCTGTTCTGTTCTATGCCTTT TGCTTTTAATCCATCACCGATC	p000801	D	--
<u>120</u>	IM000738	GAATGTCTAGATGGAGACTGGACAGAGT TGGATTCTAGACACCTAACAGAAGCGA AAGCAGGGGATGGATAAGGTGGGTGCC TCGTCTACAGCAGGTTCTGAGTGTCCG CAGAGACTCCCATGGCTTGGCACCATGG TTGAAGCTTTCATCGATC	p000803	C	--
<u>121</u>	IM000739	CTATTTTCGTTCTCTCCGATC	p000804	D	--
<u>122</u>	IM000740	GATCCTCATGTCAAGGCAGGGGCAGAC CAGGGTCAAGGGAAAAACACCTGCTTTC CTGGGTTGTAAATGCCAGAAAGGGAAGG CACGGGGTGGGTAGGGTGGAGAACATG GCCCAGACCCCTGTCTCTTCTCT	p000806	D	--
<u>123</u>	IM000741	GCACCTGACTTCCTCATATAAGACACAAA CATCTTGAGTGCTGCGCAGGTGTACCAG GATACAGGTGAATCCAATCTGGTGGAGA TTTGCCCCTGCTGCCCTGATTAGCTGAA GCTGCGTGCCTGGTGAGGTGGCATGGC CTGCTGTGCGTGGATGGGAAGTGAAGT ATAAAAGAGCGAGAGGCCCGGGTTAGA GGAGGATTATTATTCGAGAGAGGATTGT TATTATTGGGAGATATGAACAAGGGAGA TATAACAGGGGAGATATAACAAGGGA GATATATGGAGAAAGAAGAACAGGACT GAATAAATGTGTGCAGAAGGATC	p000808	R	--
<u>124</u>	IM000742	GATCCTTCTCCTGTCTTCTTCTGGAAG GCTGGGCTACATGCCAACATGTCAGAGT TTTACCTGGGTTCTTCCAGAGGTTTGA CTCAGGTCCTTGTACTTACACAGCAGCT ACTTTGCCTATTGAGTCAATATTTTGTGT GTGTTTGTGTAGGTGTGTTTCATGTCTGTA TACTTG	p000809	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>125</u>	IM000743	GATCGTGCATGCATGGGTGTGTTTGGG GAGAGGTTCTGTCCTTGCTAAG	p000811	D	--
<u>126</u>	IM000744	AGCTCAGCTTGTCAGGCCTGATTGTGAA CACTTCACCAACCGAGCCATCTCGTCAG CACAGCCCTGTTTTTATTCCCATTCT TTTCTGTATTCTGTTGAATTTCTCACATA CTCTCCTTTCTCTTCTGCCTTCTTCTGGT TTCTGCATCATTTCTATATTGACATTTAAA CAACCCCCAAAATTCAAGATACATCAACA AAAATTTATTCAACTAGTCTTTCTTACTTC CATATCAATAATGAAAGAAAATTTAAACC TTTCAAATTCACAAATCCCTACACTACA TATAATCACTTTCCTCTATGCTAAATCCA ACTTGAAATTATATCCTCAATACCCTGCT GGTATTTTACTGTCTACATCACTGCCTA GTCTTCGATC	p000812	D	--
<u>127</u>	IM000745	CTGGTATATGAACGAAGTTGGTCTCTAAA GGCCGTCTAGAACAACGTTCTCAACCC GAGGGTCGCACCGGGGTCACCTAAGAC TACTGGGAAAGCACAAATATTTACATTAC GACTCATAACAGTAGCAAAATTACAGTTA TGAAGTAGCAACAAAAAATAGTTTTATGG TTGGGGATTACCACAACATGAGGAACTG TATTCAAGGGTCGCAGCATTAGGAAGGT TGAGAACCACCGATC	p000815	R	--
<u>128</u>	IM000746	TTCTAACCTGCTAGGGTTTTCTCACGTG GGTTCTTCTTTGAGGGCTCTCTGGCTTC CCTACTGAGCTGTAGCTGCCAAAGTTGA AGGGCTGCGTCTCCCTTGCGTCTCCCCA GTCTTTACAGCTCCTGAAACACACTAAG GTATTTATTCAAATCCCTGTTTTGTGTGC GATC	p000819	D	--
<u>129</u>	IM000747	AGGGCCCTTCCACCTCTTCTAGAATTG GTAAGCTAAAAGTACATGTATCCGATTAA TCTGAAATAATTTGTAGACAGTTTGGTG ACGGGTGGAGGGTGTGTGGTTGCGCGA TC	p000820	C	--
<u>130</u>	IM000748	GATCGGCGAGACCACGATTCGGATGCAA CAGCAAAAGGCTTTATTGGATACACGGG TACCCGGGCGACTCAGTCTATCGGAGGA CTGGCGCGCCGAGTGTGGGGTTCGGAC CAA	p000823	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>131</u>	IM000749	TTGGCTGTGGAGATGAACGTGGGAACC GTGGAAATGACCCTAGAATGGGGCTCAA ATGTGAAAGGCATGCCAGAGGTTGCTCT GTTGTTTTAAGTCCCTGCCGAACATTAGA ATTTAGCCTCAGTTTTAAAAGCTGTTACT GCCTAGTTGGGTGCTTCTTTCTTAAAAAG CAACCAAAAAAAAAAAGCCGTTTTCACT CTGAAATGTATTAGAAATTTGCATTAGCC CAATGGCTAATAAGCGATC	p000824	D	--
<u>132</u>	IM000750	GTTATAAGGATTGCATACAAATGGCATCA GGACTGGATGTGGTGGCACATGTCTTGT ATCACAGCACTTGGTGAACAGAGGCAGG GGAATCTCTTTGAGTTACAGGCTAGCCA GCATGACACGGTGAGACTCTGTCTTAAA CAAACAAACAAACAAAAACAAACAAAG GTAGCATAAGAGCGATC	p000825	D	--
<u>133</u>	IM000751	ACCTGAATCTTGAATAATGGGCTGTTTT CCGATC	p000827	D	--
<u>134</u>	IM000752	AACTAATACCTTTCTTCCGCTGCGATGT TTCATGAGACTCTGGGTTAGTGCATGGT CAGGGGCCAGGCAAAACAGTGGCAGTT CTGCCCAGGATC	p000831	D	--
<u>135</u>	IM000753	GTTTAAAGAGCCGGTTCGACCCGCTTTC CGTTTCGCTCCGGGTGAGCTAGTACTGT GAACCGCTCGGTGCGGTCCGGCGCTGC TGCGCACCTACTCGCCGGGACCCTGAA GCCCCCAACTACATATAGGGGTCTTCC CGGAAAGTACGCAGGAAGTCGCGTTCG GCCCCCTCCCCCAGCACCAACCCAG TCCCTTCCACCCCCCGGGATC	p000832	D	--
<u>136</u>	IM000754	GATCCCAGTAGAGACAGAAACAGTGCCT TTGGTTAAGAATTCCAGGCAGGATGGTA CAGGATTGCAATCTCAGCATGGGAGACA GAGGCAGGATTTCCAGGCCAGCCTGGG CTACAGTATAAATGGGACCCTGTCTCAA GTAATTGAAAAAAAAACAGAGAAAGAATT TGGAGACTGTGACTATAGCTTGGTGATG GAGTCCGTTTGCCTAGCAGAGTGAAGCA GCTGTGCTCCTGTGTTACACCACAAAA TAA	p000833	D	--
<u>137</u>	IM000755	GATCCAGTGAATCTGGGCATTGTGAGTG TGTGACACAACCTTGCTCTATGTGCTGTTA GGGATTTGTGCATGCTCAGCCAACAACA ACCGCCAACCTAGACTGATGCTGTCCCC CTGAGAACACAGACTGACAA	p000834	B	Mm.1313 36

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>138</u>	IM000756	GATCCTCCCTACCGGTCCTCGGGCAGAC CTCCAGCCCTTCCCCAGACACTGTTGGA AAGCAGGCACGCCTTCCACAGTATGGTC TGAGGTTAACCCATGACAGCACTCTGGG TGCCTGGTGGTGTTCCTGGTGGGGACG TCAGTAGCTGTAGCTCTGTCATTGGTCC TTGCAGCGTCTCATTCCAACATTCTTCC CATCACTCCTCT	p000835	D	--
<u>139</u>	IM000757	ATATGTGTTTGTGCGTGTGTGTACATGTG CATGCATGGCATGTATGTACCCATATAAA TATGTGTATGTGTGAAGTGCTGATGTA TTTACACAGCATTGTTGATTTAATGGAG AAGGTAGCTCAGATGTCAAGTGTGCCCT CCTGTCAGGAGAGGAAGCCTGATGTGC CTGCTGTCATAACTCTGGTTTTGATAAAT ACAGCACGAGTGATTTTGGCTGTTGGG TTGCCGTGTATGGATC	p000837	D	--
<u>140</u>	IM000758	GTTTGCTTGCAACATTGTCATAGCTTAGT GAACAGTATAGCATTGTTCTGGCTCAAG AAGCCCTGGTCTTCAAAGCTCCTACTTA GATGAAATTATTTGCATCACAACAAAA TTGTTTTGCATTTTTAGATAATGAAGGA TC	p000838	C	--
<u>141</u>	IM000759	GATCCTAGGCCAGTCAGGGCTACCAATA AGAACCTGCCACACACACAAAAGGAAAG CAAATTTTGCAAAACTCTAGTCTCATG GTGTCACGGTCTTTAAACATCTTGAGGG GCTCGAACTGGTGAGGTGGCTCGGAGG TAAAAGGGCTTTGATGCACAACCTGAGT TCAACCCCGTGTTTTAAAGACTTTCTGCA ATGATTCTGGTCTGCAGTCCTAGCCCAA GCACAGTCAAGGAGAGATTGAGGCTGAA ACGGAAGAATGGAAGTTGCATAACAGC TCAGTGGCAGAAATAACAGGAGAGACCT GACCTTAAAAACAGGGTGTAAAGGTGAGA AATGATGACAAATGACATCCACTTCAACT GTGCTACGAACAGCTACCTGTTTGCACA CCCCAAACACACACACACACA	p000839	D	--
<u>142</u>	IM000760	GTAAGAGGGAATGTACTCTCTGCCATCG GGACACCCAGTGGAAGTCTCACCTGGA GTCTTGCTCCACGAAGACTAGGATC	p000840	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>143</u>	IM000761	GGGACTTCAGGGCATAGAGCTTAGTTCC AGACAAAACCAAAGTTAGCAGTCGCCTC TCTCTTAAAGACGTTCTCTCTAGCCGCA GATGACCTCAGAAGGGGCTCTGGGAGC CGACTCCCACCCTTCCTTCTCTGTTTACA GAATCTGGTTGGGCTGTGAGGAGCGAC CCACGAGACGGGCTCCCTGTAGTGAGTT AGGCCAGTGGGGAACCAACGAGGATC	p000842	D	--
<u>144</u>	IM000762	ACACACACTAACACACACTCACTCACAC ATACTCACACACTCACACACTGTCA CACACACACACACACACACACACACA CACACTTTTCCACCAGGATC	p000843	R	--
<u>145</u>	IM000763	GATCCCTGGATATGGCAGTCTCTACATG GTCCATCCTTTAGTCTCAGCTCCAACTT TGTCTCTGTAACCTTCCATGGGTGTTT TGTTCCCACTTCTAAGGAGGGGCATAGT GTCCACACTTCAGTCTTCATTTTCTTGA GTTTCATGTGTTTAGCAAATTGTATCTTA TATCTTGGGTATCCTAGGTTTTGGGCTAA TATCCACTTATCAGTGAGTACATATTGTG TGAGTTCCTTTGTTCAAATTTCAATTCAT CACCATTGTGTGTATATGTGTGTGTTGTG TGTGTATGTATATGACGTGTGTATGTTGT GTGTGTATATATAACGTGTGTATGTTGGG GGTCAAAGGCATGCTCATGCCACAGTGA ATGAGTAGACATCAGAGGACAACCTTCA GGACTCAGTTCTCTTGTCTACCTGTG GTTCCAGGACACTAACCAGGTCATCAG GCATGGTGACAAAGGTTTTGACTCAAGG AGCCATTTTACATGCCTCATAAGAAGGG CC	p000844	R	--
<u>146</u>	IM000764	GCACTAGGAAGGAAATTGACCCGTGTTG TTGGTTTGTGTTCTGGTTTTGTTGGTGGT GCTTTTGTGTTTTTGTGTTTGTGTTTT TTGTATCAGGATC	p000845	R	--
<u>147</u>	IM000765	GATCCTGCTTTCTCTTTTGACACAGAACA CTTCTCCTGATTGACTCTGGTCCAGACAT TTCTTTCAAAGGCAGAGGACTCTGGCTT AGCTGTGGATGACTTCTCAGATGAAGTT CATTGGTTGCGATTGGAAACGTAATCAG AGCAGG	p000847	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
148	IM000766	GATCGCATTAGGGTTTTTTTATGGTTTC TCATCTTCTCTTCAAATTAGCATAGAAGC CTCTTCCTAAAGAATGGATACTTAATTCT TAACTTGAAAATATCTTTTCTCTGTGTGT TTCCTCTCCATTGACTGTTGCTCTATCT ATCTATCTATCTATCCATCTATCTACTGA AATTAAAAATAAGGGAACGCCTTCTTCTC TTCATTCTTGTTTGTTGTTTGTTTGTTGT TTGTTTTTGAGACAGGGTTTCTCTGTGTA GCCCTGGCTGTCCTGGAACCTCACTTTGT AGACCAGGCTGGTCTTGAACCTCAGAAAT CTGCCTGCCTCTGCCTCCCAAGTGCTGG GATTAAAGGCGTGCACCACCACCACCTG GCTCTCTTCATTCTTTTAAAACGATTTT GAAACCTTTTTAGTGAGGTCAACATTGTG TACTCCAGTCCCACTCATCTTCCTGTCCC TTCCCTCTTAGGCCTGCCTGTCTGGTAC CTCACTCATGTTTGTGTATTCTCTGTGCT GAGCCTCTTCTGTGCTTCCAGCACAT GGCTGCTGGCTCCAGTTTCATTCCAGTC CCTTGATGTGAGCCTAGTTCAG	p000852	R	--
149	IM000767	CTCTCATGGCATGGGTCTCAAGGTCCTG CCATTTCTGCTCCATCTTTACCCAGCAC ATCCTGTAGACAGGACAAATTGTAGGCC GGAGGTTTTGTGGCTGGGTTAGAGACCC AGTTTCTCCACTGGAAGCCCTGCCCGGT TACAGGAGGTGACCAGTTTCTGGCTCCA TGTCCCCCATTGCTAGGAGTCTTAGCTG GGGTCATTCTCACAGATTCCTGGGAGAT TACTCTATTTTATCTCCTTGTTCAAAGTGT TCCATCAGATATTAATTATTCTCAAGATT CAATATTCTCAAATATTATTCTCAAGCTAT GGACCCTTCAAATTACAGATAGATTTTAT GAATGAAAAGTTGTGTGGTTTGAATATGT AGTTGAGGGTGACTTTGAACCTCTGGTTT TCCTGTGTCTACCTTCCAAGTGCTGGGG TTACAGGTATGAGCCATCACGCCAGTTT CTGTAGCACTGAGGCTCAAACACAGGGC TTCTGTCTGCTAGGCAAGCACTCCACCT ACCAAGCCAAATCCCCGGGCTTTACTGC ATCTTTGTGTGTATATGTATGGTATGTGC GTGTGTATGTAAGGATATATGTACCTGTG T	p000854	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>150</u>	IM000768	GATCAACACCTGAAAAGTCGCGCCGCCT ATACACATCCCTAATTGAGAAGTATGTGG AAGATTCCATCCGTGAAATTCAATTATCA TGCAAGCCAAGTGAAGCGCTTCCCTGG GGAAGGAACCCAGCAGCCGCATCAAAA CGACCCACCTGTCTATTTTCATGTCAAA AGAGTGAGAAGTCTGGGTGATGAAATAG AGAGCATACATCAGCTTAATGAAAATTC CAGGGGTCCCTGCCTGTAATGGGAGTC CCAT	p000858	D	--
<u>151</u>	IM000769	GATCACCACCAGGGTGTTGAGAAAAAAA AAAAGCAAGTTAGTAGATGTTAG	p000860	D	--
<u>152</u>	IM000770	GATCTGACAAAACCTACCTGTTTTGAAC ACATGTGGGACAGCAGTCTGAGAGAATC TATGAATAAAATTCCTTCTGAGTCTGGC ACATTGGTACAC	p000861	D	--
<u>153</u>	IM000771	GATCATTATACCCCAAATGGTACTGTATC TATATACCTCAAACATGTCATGTTAA GAAAATACTCTGTTGAACTAATCACTTG TTT	p000863	D	--
<u>154</u>	IM000772	GATCACAGGACTGAATCACATTTATGCC AT	p000864	D	--
<u>155</u>	IM000773	GATCATTTATTTACTTGTTTTGGTGTTC TGTTTGTGGCTCCTTATGTAGTCTAGATA TTAACTTGAAGTCTGAAGTGGAACACCA AAGATTTTCTTCCATCCTCATCT	p000865	D	--
<u>156</u>	IM000774	GATCAACCGCAGATGAGGTCTATGCAGG AAAAACGATGTCTGGAATTTATTAAAT TGCTCAGC	p000866	K	<i>Myc</i>
<u>157</u>	IM000775	GATCATCATGTCAAACCTGACACGTGAC GAGACAAATCTGTGTGCACAGAGGTGTG ACATCCTAAAAGTACTAACAATACCGCTG GGCAGGGACACACGCGGCAATTCCAGT CCTGGTATCCATGGCTCAAGCTCTGCAC GGAGAGCCCGGCACACGGCAGGAGGGA GAGCCACAGGCTAAGGAGAGCAATGCTA ACTAACATGGCACCCGTGTTAG	p000867	D	--
<u>158</u>	IM000776	GATCTGGCTTCCAAGGGCCTGTAATCAT GTCTACAATGCTCCTACACAGATATAT	p000868	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>159</u>	IM000777	GATCAGCCTTCCTCCAAAGCTACCTGCA TAGAAGAGACCTCTGCTCTCACCTACTC TCCTCTACAGTTAGCCCATATGGCTTCA CCTGCATCCCCTACACACACACACAG ACACACACACACACACACACAAACACGC ACACAGCACACACAACACACACAACACG CACACTCACAACACAAACACACACAACA CACACTCACAACACACTCACACACACAC ACAACACACACACACAACACACACTCAC AAACACACTAGTACACAAAGACTCCAAC ACACACATTCCCATGCACTACTCCCTCA GTATCCGCCGCATTTGTGTTCACTCAT CCCACTCTCACACATGTAGCACACACA CATCATTCTACACAGGCATGGACACAC ACATGCTCCTATACAGGCATGCCAGTA CTCTCATATGCATGTTTGCACGTTCCCAA ACAGGTTCCCAAGGGTTTGGCAAAGT ACATGCATCCTCACACGCTAATGCAAGC CGTCACACCCCATACCACAAGCATGCAC	p000870	R	--
<u>160</u>	IM000778	GATCAGATGTGGAAATTAGAGAGAAGTT TTTAACGGCTCATGCACATTTCTGAAAAC TCTTTGCGAGGTATACTGGTAGATAAATG AACATTGGTCAGACTCCTCTAGTTTAAAC CACTCTCTTCCCGCTATGGGGGGAGG CGAGAGGCATTTCTAAAGCTTATATGTAG TTGCAAAGTGTGTGTGGTGTGTGTGCAT GTATGTGCATGTGGTGTGTGTGTGTGTG CATGTGGTGTGTGTGCATGTATGTGCAT GTGGTATGTGTGTGAGTGGTGTGTGTGC ATGTGTGTGCATGTATGTGCACCGTGT GTGTGTGTATGTGTGCATGTGGTGTGTG TGCATGTATGTGCATGTGGTGT	p000871	R	--
<u>161</u>	IM000779	CTAACATCTACTAAGTTGCTTTTTTTTTT TCTCAACACCCTGGTGGTGATC	p000872	D	--
<u>162</u>	IM000780	GATCATAAGGACTGTTAGCAGGCAAAGG CGCGTGCCCAATTAAGATGGCTTTTCG TTCCAAGAGGAATACTCTGGCAAAGTCC CAAGCGCTTCGGAAGCCCCTCCCTTCGC TCTCCACCCCAGCTTTGATGCTCTGATT ATCCTAA	p000874	D	--
<u>163</u>	IM000781	GATCAGGCTGGCCTTAACTCAGGGAGA TTCATATGGCCCTGCCTTCAGGGTGCTG G	p000875	B	Mm.8363 5

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
164	IM000782	CTTTCTTTCTTTCTTTCTTTCTTTTTTTCT GAGACAGGGTTTCTCTGTATAGCCCTGG CTGTCCTGGAATTCAGTGTAGGCCAGGA TGGCTCAGTCTGCTTTCTTATAGAACTCA GGACCACCAGCCCAGAGATAACACCACT CACAGTGGGCTGGTCCTCCCCACATTGA TC	p000876	R	--
165	IM000783	GATCACACACTTCACTGTGGCTTGTCAA CTGTGATTTGCTGATACAAGGGCTGTTTA CAAGTCAGCTATAGCTCCGCATTGCAGC TGCAAC	p000877	D	--
166	IM000784	GATCACTAATTGAGAAAATGCCCCACAG CTGGATTTCTGAGGTACTTCCCCAAC TGAAGCTCCTTTCTCTGTGATAATTCCAT CCTGTGTCAAGTTGACAGAAAACCAGCC AGTACACAAGTCGACACAAAAGTAGCCA GTACACAAGTCAACACACAACGCGCACA AGCTGAAGGCAAAGAGAACCAAGCATCT ACCAGGCCTCAGTTGCTATGTCCACTTC TGCAGCCACTCCAAAACACCTGTCAGAA ATTTCGTTTGATAGAGAACTCACCGAGG GATTTCCCTAACACCAGGTCAACCAGGG CACCTCAAACCTGGAGGCACGACTGGCA CAATACAACCTAA	p000878	A	Cct5
167	IM000785	GATCACTTGATAAAGATGCTCTGAGCAG AGGCTCACAGGAACCCAGCCCTGTGTG CTCCCCAGGAGCGAGATTGAGCAGTCAA CAGTGCAAGTGTTCACGTGACCGTGCGCA GGCCATGAGCACTAC	p000879	B	Al615991
168	IM000786	CTCCTTTTCAGCAAGCTCCTCACATCACA GGCCTTCTCTTGGGATGGCAGCCGCCTT CTATCTGGAAGTATGTGACAGCTCACA CAATCCTGTAAGTCTTCCATGTAATCACA TTCCACTGCCTCTCTGAACGTGCTCC ATGCCAGGGCCATGTGGAGGGAGCAGC AAGACTTGAGCTCAGCTAGTCTATGAAG ATGGTGGCAGAACAGGCTCTGCTGCCTT GATC	p000881	B	MMU767 54
169	IM000787	GATCAAGAGTTCAAAGTCATCTTCAGCTA CAAATGAAGTTGGAGACCAATCCAGACC CTCTCTCAGAAAAAAGGAAAAAGGAGA AAGCAAAAGGAAAGGAGGGGAGACCG AGAAAGAGAAGAGGGAAGGAAAGGGAA GTCAACAGAACTCAAGGTCAGCCTGGGA GGGTGAATGAGGCATTGTTGTCT	p000882	B	Mm.1388 09

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>170</u>	IM000788	GATCACCTCCACTTTATGGTGGACAGAG GATGGCAGTAGTAACTGCCCCAAGGAAA CAGAAACAACAACAACAACAACAAC ACCTCCAAAAAGACCAAAGCAGTAAGCT GTAGAACAAATGCAAAGAGCCAAAC	p000883	R	--
<u>171</u>	IM000789	GTTCCACCTATAAGGTTGCAGACCCCTT TAGCTCCTTGGGTACTTTCTCTAGCTCCT CCATTGGGGGCCCTGTGATC	p000884	R	--
<u>172</u>	IM000790	GATCACATGGACCGATTGCCGCGGGAC ATCGCACAGGAGCGTATGCACCACGATA TCGTGCGGCTTTTGGATGAGTACAACCT GGTGCGCAGCCCACAGCTGCATGGCAC TGCCCTGGGTGGCACACCCACTCTGTCT CCCACACTCTGCTCGCCCAATGGCTACC TGGGCAATCTCAAGTCTGCCACACAGGG CAAGAAGGCCCGCAAGCCCAGCACCAA AGGGCTGGCTTGTGGTAGCAAGGAAGC TAAGGACCTCAAGGCACGGAGGAAGAA GTCTCAGGATGGCAAGGGCTGCCTGTTG GACAGCTCGAGCATGCTGTGCGCTGTG GACTCCCTCGAGTCACCCCATGGCTACT TGTCAGATGTGGNCTCGCCACCCCTTCT TCCCTCTTCATTCCAG	p000885	K	<i>Notch1</i>
<u>173</u>	IM000791	GATCATACGCAATGATTTCTTACCTTATG ATATAATTATGTTTAGAGGGAACCTTTT TTTTAAATTGAAGTTCATTTATTGTATGAA ATTATTCATAA	p000886	C	--
<u>174</u>	IM000792	GATCAGCATGGTCTACAGAGTAAGTTAC AGGACAGCCAGGGCTCCGTGGAGAGAC CCTTTGTCAGAAAACAACAACAAAAA TTAGAAAGAGACCCTCTCTCTGATTTGAC CAATCACCCGTGTCAAATCTTGCCACAA CCGAATCACCACCAAATTGCCAGACAAG CGGCTATGCTGGGTTTCTGAGGTTGGAC TCCTCAGGTAGCCCGTGTCTAGGCAGAA TGATGCCAGCAGCTACACTTTTGAGAAC AAGGTCAGGTCAGGACTTGCCGCCAAAC CTAGGAATGCAGC	p000887	R	--
<u>175</u>	IM000793	GATCAGTCATGTCCTTTAGACGTTTACTT TCATCCCACTTGGAACATTTCAGC	p000888	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>176</u>	IM000794	TTACAAAGGCAGAAATATCAGAAAGAGC CTGAAGTAGCAGCTGTTAACCTGTACCA GGAAGTGGCCGAAGTACACACGCGTTAA CTCAGCCCTAATTATTCTCGGGAGATAC AGTTGATTATCATACACATGTCAAAATGG AAAATAAATGGGTAACTAAAAATTGAGGA AAATAAGATTAACTTAACAACCTAGT TCATTATGCCACGGTGATC	p000890	D	--
<u>177</u>	IM000795	GATCACAGTGGGACAGATTAAATGTTA	p000891	D	--
<u>178</u>	IM000796	AAACAAATACAAAGTGATAATTGTGTGAC ATCTGAAGTTGTCAATGAGATAGGTAATT ATCTCTGGGCAATGGGTAAATGTGCTGG CCAGCAAACCTCACAGCCAGAGTTCAAT CTCCAGGAACTTAGGTGGGGAAGGAGAT AACTGACTTCAAATGCTCACCCCCAAAT ATACAATTAATAAATAAATCTTCCTTTTAT GAGTAGCAACTGATC	p000892	D	--
<u>179</u>	IM000797	TACCCCTGGTCCTCCAACACTCCGATC	p000893	D	--
<u>180</u>	IM000798	GATCATGACATAGACTTGAGTCACTTCTC TGCAGTTTGTCAATAAAAGCCCCTAAGG GACAGTGTGGACTTTAGAGATAAC	p000894	D	--
<u>181</u>	IM000799	AATGCCAGCCATAGTGGCACACACTTTT AATCCCAACACTCAGGAGAAGTTAAGTTT CTCTTAGCTCAAGGCCAAGTAGCTTGGT CTACTCCGTGAATTCCAGCCCAACTACA TAGTAAACTAGCCTTAAAAAAAAAGGCA CAGGCAGAGGGAGATAACAAAAATGCC AACTCCTAGCTACAGTAACTGTAGGAATT AAGATAGAATCTGTAGTTTGTATCATT ATCGTGATGATC	p000895	A	<i>li</i>
<u>182</u>	IM000800	GATCATGGCTTGATTGTAACATTATCAA GCTTCCTTGGCACACTGCAGGGCTGTCT TCGGGAAACTGCGTATTGTGCTCTTCAG GTACAAAGCATAGAGCCCTTACATGACA AACGCTGGGGTTAACTTCTTCTAGTTCC CTCTGCCCCACTTGTGGCGCTTCCCACT CATGACTTCTTCAGTGTGTATTCACTT	p000896	D	--
<u>183</u>	IM000801	GATCATGCTGAAGTCTTGAAAGTATTCTA GCAAAATGTGGCTTAAAGAAAGAACAA ACATTAAGTATGCTTTGAAAAATTA CCTGTGGTAAATTTCCACAAGCATGAG AAGTTGTTTCTTTTGTGAACCTTCAGAC	p000897	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>184</u>	IM000802	GATCATATATCAATTTTATTTTAACTTTG TTTGTGTTGTTGTTGTTGTTGTTGTTGAG ACAGGGTTTCTCTGTGTAGCCCTGG	p000898	R	--
<u>185</u>	IM000803	ATTGTGTATCCAGAGTGTGACAAGGTAT ATATGGTTGTGTGATC	p000899	D	--
<u>186</u>	IM000804	GATCTTCTGTCTGGAAGAGTGCTTGCTG GTTCCGACTACTTTTTTTTTTTTTTTTTT TTTTNGCTTGGGTTTCANATTGGCTTCAG GTTCTGGGCCCTTTCGTGGGTTGTGCTG CANAGCCCCANACAATGTCTTGGG	p000900	R	--
<u>187</u>	IM000805	CAGGAAACCAGGGGAAATGGGACACAG TGACATCTGAGTCCTTAGAAGAGGTCCC ACAAAGGTCTATATGACCTAGCAACGTC ACTTCTGAGTTATTTCTCAGACACAGTGG ATGTTTGTCACAGCACACTGTAGGACAT CCCAGAACAGCACCATGGGAGACCATG GTTGGTGCAACAGAGAACATGCACACTG AGACAGTACAAGAGTTCCCAAGCAAGCA GACACAAACAATGGACTCAATACACATA CAGTGGCAGATC	p000902	C	--
<u>188</u>	IM000806	GATCTGCTCACCAAAAATCTTGTCTTAG GGAAGTTGAGTTTGAAGTGCCTGCTTAC TGGCAAAACACGCGGTGCCCAAATTTAAA	p000903	D	--
<u>189</u>	IM000807	ACAGTTCCCCCTGGAAATGGTCCCTGTA CCAGAGGAGCAGATC	p000904	D	--
<u>190</u>	IM000808	CTGGGGCCCAGACTCCAATCCCGAAATA TCATTAGCTGCTGCGCACTTCTCCGAGG AAGTTTACACCAGTACCCTAAGTTCAAGT CTCAGAAGCCTCCAAATCCTCGTTGCAC CCCTATATTTCACTTGGTCATCCGACTGT AACTCACTCACCGACAAGACAAAGAATA TCTTAGGCTCCGTCGTAAAAGAACGAGC CCGGTTCACCGCAGCTCCTTTTATAGTC TCCTTTGTGCGAGATC	p000905	B	Mm.2179 8
<u>191</u>	IM000809	GATCTGAAGATATTTTGACAACAGCTAAA AAAAAAAAAACCAAAAAAACCCCTTATT ACTAACCAAGGGAAAAATGCAAAAATAATT AAAAGTTCCTCAATTTTAAGTAAATATCC AAAAAGATTGGTTGTATAACAAAGTTGAA GAGTCAAACAGTATTTGAATAA	p000906	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>192</u>	IM000810	AGCTCATTGCCGTTAATTTTCCTCAGCCT AATGAGAATCTAAGCCTTGATTTGTATGT ACCATAGCATCTAGATC	p000907	C	--
<u>193</u>	IM000811	CCTTGAACCTAGTTCAGGGAATAGGCCA CCTGGGTGGGACTAGTGCTGGTTGGGG ATGAAAAGACAGTTGGCTCAGGTGAACC CTGCTCGCACCCCTGGTCATCCTCTGAGA CTGCTTTGATTGCTGACCCCACTGCTCC AGCAAGAACTTGC GTTCTTGTCTCTCCA CTCAAGCCGGAAGAAATCTGAGGAGAG GGTGTGAATCCTGAGCCAGGATGTCCAA AACAACGGAGTTGAGCCAGAAGGACGTC TAGTTGGGCAGAGTTAGCTCAGTCCCCT GACCCCACTCCGTGCAAGCTCGAGGG TGTTATATAGTGATACAGATC	p000909	D	--
<u>194</u>	IM000812	GATCTCTTCTTATCTCTACCTTTTGGGGC ACAATCTTATCTGGGGACACCACAGAGC CCAAGAATTGTCCTGTATCAGAAATTTGG ACCTTTTCTGTGGCTATCTGTAAACCCCA CTGACTTAAAGTTTTAAGTAGAAAAGGAT ATGCCTTTTGTAGCATGGTAAGGTCTTTA TGGCACAGGAGGATGTCATCCATGT	p000912	R	--
<u>195</u>	IM000813	CTTCCTTTCTTTTTTGAACAGGGTTTC TCTGTGTAGCCCTGGCTGTCCTGGACCT CAATCTGTAGACCAGGCTGGCCTCGAAC TCAGAGATC	p000913	R	--
<u>196</u>	IM000814	GATCTGCTCCACTTTACACAGCTGACCA TGAGACCATGTNCACATAG	p000914	D	--
<u>197</u>	IM000815	ACATGACATATCACCCCTATTGAGAGTTC AGAGTCTTCAGAAAACCTGGGCGCCTGAA AAACCTGACCTTTTAAATTTTCGTCCATA GTTTCTTCTGTTGAATGAATATTCATTTAA AAGCTTCATAAATGCCAAGATC	p000915	D	--
<u>198</u>	IM000816	GATCTTCACAGCGCACCCAGGGATC	p000916	D	--
<u>199</u>	IM000817	CTTTTTCTGGTATTTAGGGAGTCAGGAA AAGAAAAACCATTGGGTTTTTACATTAGC TTTCAGGTAGGGTTGTGGCTTTTGAGCA ACAATAACGTATGACCTTGTGGTCGGTT CTAGATC	p000917	D	--
<u>200</u>	IM000818	GATCTTCTTATATCTGGTTTCCTGGGCGC TTCCTGGTAT	p000919	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>201</u>	IM000819	GATCTCTGACAGGGTTTCAAAGAACTGT TACTGATGTTTAGATTGCCTCTGAAGACA TCACATATACTGTGCTACTCTGCCTTGTC AGAGTCCCGGGCCCTGGGCACCCCAGA CGGCAGCAGAGGAAGAGCGGGGTATCA CTTTCTATACTTCGGTAAAGTCATTGGGA TATGTGCCCT	p000920	C	--
<u>202</u>	IM000820	GATCTCCTCTATCATTTATCTTTCTTCCTT CCTTCCATCTGTTTGTTT	p000921	D	--
<u>203</u>	IM000821	GATCTGCTCACCAAAAATCTTGTCCTAG GGAAGTTGAGTTTGAAGTGCCTGCTTAC TGGCAAACACGCGGTGCCCAAATTTAAG GAGTGCCAACGACTTCGCGGGCCAGCA AGGTGAAACCGAGCGCGCACGAGTGA GCAGTGGCCAGGAGGCCTGGCCAAGAG GCCAGGGTCCCTGAGCATGACCGAGAG CTGGCGTGCTCTCTGTAACCCCAATCA GTTACCTAATCTCGGGTCGAAACCTGA GCCCTGCAGGAGGCGGGGCTGAGACTG CATCCAGCTCCTGGCCCGCTCCAGGG GCGACCC	p000922	D	--
<u>204</u>	IM000822	CCAGGCATCTCCATTCTTAATCCAGATC	p000923	D	--
<u>205</u>	IM000823	CATAGACTCTTTCATTTAGAATAAAGTGT TCCACCTAACATCCTGTAGGAAGTGATG AAACTAAAAAGAAAAATAAACGCATTTTC TCTTTCTCTCGTTACTTTTTCCATTCACTA AACAAAATTGACTTTTTTTTTTCCATGAGA GTTCACTGCGGTCTGCCTCAGTAAGAG TCACACTGTTTCAGCCACACACGCTGTG ATATGTTATTTACTCATTCTCTTCTCAGG AACCCTCTCACATGTGAACCCTGAATA CCAGCTCCCTCCCTCTTCAGATC	p000925	D	--
<u>206</u>	IM000824	ATAGGTTCTGTCTCAAAACAAACAAAAA CCAAAACATGTCCACAGGGTCCAACAGA CACAGTCTCCGCCACTCACAATAATGG GTACACAAATACACACCTCAGCCTTACAT GGTTACAGAGAGAAGCAGGACCACAAG GTAGGCAGGCACCTAACACTTGCTTCTT GGAAGTTGGAGCACACACACACACAG AAACACACACACACTTTCTCACACTCACA CACACATTCTCTCTCTCTCACACACAC ACATGCACACATGGTCTTGTACAAGCTC CTCCTGGGATGGGCACACACAGGGGTA AGAGGACTCCAGATC	p000926	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>207</u>	IM000825	GATCGAACACNCTNGGACTTGNTAAACG NTTCCACACNGACAGA	p000928	D	--
<u>208</u>	IM000826	GATCGTCTGGCCCCGACCGCGCCTCAGT AGATTGGGTCTGGTCTGAGCAGCCGG GCTGGTGCGGTGTCCTCACTAGGATAA TGAATACAGCTCCACTACCTATACTACCC AAGACGACCCCTCACACGCTCTGCGAG GAAACCGGTCTTCGGAC	p000930	D	--
<u>209</u>	IM000827	GATCGACCGCAGATGAGGTCTATGCAGG AAAAACGATGTCTGGAATTTTATTAAAT TGCTCAGC	p000933	K	<i>Myc</i>
<u>210</u>	IM000828	AGTAGACTGAGATTTGTGAGCGCTAAGA TAAAGATGAGCAAAGCTTTGGCAGCTCT TAGGTATCTGAGGGCCACCGTCCTCTAC AAAGCAACGAGAGGCACGGCGGATTAG GATAGACTGGTTGCATCCAAACACTACC TTGCTGCCTCAAAGGCTTATTGGACACC ACAGAAAGACCTCTGCTGGAGGCAGAAG TCACAGGACTCCTCGTCACAGACGATC	p000934	D	--
<u>211</u>	IM000829	GATCGGCCTTCCTCCAAAGCTACCTGCA TAGAAGAGACCTCTGCTCTCACCTACTC TCCTCTACAGTTCAGCCCATATGGCTTCA CCTGCATCCCCTACACACACACACACAG ACACACACACACACACACAAACACACAC ACAACACACACAACACACACAACACACA CTCACAACACAAACACACACAACACACA CTCACAACACACTCACACACACACACAC AACACACACACACACAACACACACTCAC AAACACACTAGTACACAAAGACTCCAAC ACACACATTCCCATGCACTACTCCCTCA GTATCCGCCGCATTTGTGCTCACTCA TCCACACTCTCACACTTGTAGCACACAC ACATCATTCTACACAGGCATGGACACA CATGCTCCTATACAGGCATGCCAGTAC TCTCACATGCATGTTTGCACGTTCCCAA CAGGTTCCCAAGGGTTTGGCAAAGTA CATGCATCCTCACACGCAAATGCAAGCC GTCACACCCCATACCACAAGCATGCAC	p000937	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>212</u>	IM000830	ACACCACATGCACATACATGCACACACA CCACATGCACACATACACACACAACACA TGCACATACATGCATACACATGCACACA CACCCTCACACACATACCACATGCACA TACATGCACACACACCACATGCACACAC ACACACACCACATGCACATACATGCACA CACACCACACACACTTTGCAACTACATAT AAGCTTTAGAAATGCCTCTCGCCTCCCC CCATAGCGGGGAAGAGAGTGGTTTAAAC TAGAGGAGTCTGACCAATGTTTATTATC TACCAGTATACCTCGCAAAGAGTTTTAG AAATGTGCATGAGCTGTTAAAACTTCTC TCTAATTCCACATCCGATC	p000938	B	Hs.17043 4
<u>213</u>	IM000831	GCTGGACCCCGGTGACAGACTGTGCAG ATGGATC	p000939	K	<i>Pim1</i>
<u>214</u>	IM000832	TTAGCAAGTCCGAGCGTGTTTCGATC	p000941	K	<i>Nmyc</i>
<u>215</u>	IM000833	ACTGCACACATTGCCGTTGTCGATC	p000943	K	<i>Notch1</i>
<u>216</u>	IM000834	CAAGTGTAGACATTGCAGGAAAAAATAT GGTGACAGTGAACAAAGCCCGTGAAGGT GACAAAAGCCAGTTAAAGTAGGACAAGG CAGAGCGAGGCCCATGACCGGGACCAG GCCCAAGAAAAATAACGAAGGCCACGAT C	p000944	B	AW32146 8
<u>217</u>	IM000835	GTCGGAGGAGCTGGCTGGACCGGTACA TGCCCTGGCCATCCAGGCGAAGACCCC CGCCCAAGTGGAGAGAAAACCCACAGTTG GACATTAGTCCCCCTGCCTAGGTGGGA GCAAGAAAACCTCGAGGGACCTCTTAATA AATACCTGGATTGGGAGAACGATC	p000946	R	--
<u>218</u>	IM000836	GATCGCGGGGCTATCTATAGAGTCCCCG GGATGTCTGAGAAATCAGCCCTAGAAAT GACTAGAAAGAAAATCGAAGTATTCTTG GCTCCTGGAGACTTCCGCAGCGAGAAGT CACAGATTCAGGACACAGATTGACAGGA GCTGCGGGCGCTGGTAG	p000950	D	--
<u>219</u>	IM000837	GATCCCAGGATTTGGGAGGCAGAGGCA GTTGGCCCCA	p000953	R	--
<u>220</u>	IM000838	CAGGCTGGCCTCAAACCTGCAGAGATGC TCCTGTCTCTGAGTGTTAGATTTAATAAA GGGGTTCACGATC	p000954	K	<i>Lck</i>

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>221</u>	IM000839	GTTGCTGGGCCCTAAGCGCCACATTC ACAGCTCCGATGCTCATCAGCATGACTC TCCTGAGCACATTATCTGGTGGTGGCTG ACACTCTCTTCAGTACCCCCCCCCCTCC CAAAAAAGAAAAAGAAAAAGGACTG GTTGCTAAAAGAAGTAAAGTCAAGTCAT CAAAAACAATGTAATATCCTGTGTGAAAG TCACGAAGCCTTGCGTTTGAGTCCCTC GATC	p000955	D	--
<u>222</u>	IM000840	GATCGGCCGGCTGTCCAGCGACCGGAG AAAGGAGAGCACTCGAATCGCAGAAGCT ATCAGGTGAGTCCGACCTCTCTCTGAAT GAACGCTTTGGGGAGCCTGCCAACGGT GACCAAATTTAGCCAGTTAAAGTACAG GCTGCCCAGCTGTAAACGTACATCAAAC AATGTGCGATTTATTTTATGTGTGAA	p000956	D	--
<u>223</u>	IM000841	ATAGTAACACTTGGGAGGAGCCATTCCC AGTGAGGCTCGTATAGCATAGCCCTGTC CAATAGAGCCTCTGTTGCACTCTGTGTA CACTTAGCTCCTTGCTTAGGGATTTTTTT TACATGGGTGACTACAGCACCCCAATTT CACATTGGACAGACTCCAGGACACCCCT CGGTGTCCTGTGACGCATACAACAGCCC CCCACGGGGCTGCACCGAAAACGCCAC AGTACTGAGGCTGCACCTCACTCACTCA CACACACCTCTATGGCTCAACGTCCTGG AGAAAAGGCTGCGACAGATTCCACATC TGGGAATGCAGTAAAAAGCACTCACAC TGGGGGTGGGGTGGGGCTGGGGGGGC ACCCTGTCTTCCCGTCTTCCCATGACCC TCTTCCCTTCCAGGAGACCATAGCCAGA GCTGACAGGAGATTCACTCGCAGCTGCA CACGCTGCTGCCTTGCCGATC	p000957	D	--
<u>224</u>	IM000842	GATCGGGCAGGACACACATTGGGGAGG CCCATCAAGCCCGAGCCTGCCTTGTGAG CCCCCGGATTGGCAGGGCAGAGAGGAA AGCTGCTGCGTGCTTTATAGACTTTGGG GAAGTCACAGGCTCCGCTTGCTTGGGG GAGGCAGGAAACCCCTCCACCTAGGC GTCTGCCAGAGCACCCGCAGGCTTCCTC TTGTCTCTGTCCCCCTCCCAGCACCTC TCCCCCTGAACAGCTTCCCTCTCCTGGC CCTGCTGTCCCTTTAAAGGAACCTGAATC AGAGTTGAGAATGATGGTGACTCAGGGT GGAAGGGGTGGTCACTTG	p000959	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>225</u>	IM000843	CCAGGGCTACACAGAGAAACCCTGTCTC GAACAAACAAACAAACAAACAAACAAACA AACAAAGTTAAAAATAAAATTGATATACG ATC	p000960	R	--
<u>226</u>	IM000844	GATCCAGGACATGGCAGAATATGGTCAT CTTCTTTGCTTGCATGTCACACGAATGG CCTCTGGCTCCACCCCTGATTGCTTGCT CCCCTTGGAAGCCTCTTGAGCCTAGCTA ACTTTTCCTGTTACCTTTGTATTATGTG CTCCCACCATGGCCCACCAGGCTCTGCT TGCAGCACTGCAGCCTGCAGCTCCAGC GGCCTTTACATGGCTCCTGTAAACAAGT CCCAGAGGCCTCAGTGTCAATTTTCAG CAACCGCCTCACTTCTTGGTGCCGCCTT CCTTTATTACTTTTCATATTCTGTGACCG AAATACCCCCAAAGAAGCTACTCAAGGA AAGCAGTATGTGTGGGCTCACCATTAGA GGTCAGTCCCCTGCAGCAGTGAAGCAT GTGCTGGTGACGC	p000976	D	--
<u>227</u>	IM000845	GATCGCTACTTTTTCAGAGACGCCTTCAT TAAGGGGAGAATGGAAAGATGCTGGTTG ACTTGAAAGATTTCTCTCTGATTGTGTTTA CAGGAAGTGCATTCTGTACACATGAGAG ACTCCGGGTGGAGAGGCATTGTGGCGG TTGAGATGCACCTGGGAGTGCCAACTGC CCCCGCTTCTACCACAGCTCTGCATAGC AGGCTGGAGCAAGCAGCCAGCCAACCA TTGTGCCCTAGCCTCATCTCCTCCAGAA GAGGTTATCTGGGCTCTGTGTAACCTCT GCTCTTTGGCTATGGTATTCCTTCTTGGT GCTTTCTGTGGTCAACCTCCAGGTACAC TTAGGGCCTATCCTAGACAGACTGGGAA GAAAGAATGACATTCCCATTGACCTCTGT TTTTATTTCTGGAAATCCAGACCTTGTT CCAGTTAGTGGAGCATGGGGTTAGACCA ACCACACTGCTAAGAGTTTTGGCCTGTA GACATATCTGG	p000983	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>228</u>	IM000846	TAGCAAGGTAAGTACTTGTCTCAATTTCC AGGTAGTATAGAAGAAACATATATGTTAC AGCTTTAACACCAGAACAATCACACAGT GTTGTATTTTAGCTAAAATATGACTCTGT GGTTTTCAAATGGCATAGTTGTGGACAA CTTAATTAAGCACGCTCTTATAAGACGTG ATAGAGTATGTGCCATCCAGATACTAAG AACTGTGTCCAAAGAGCTTGGGACACAC ACTAAGGGGCCTGCCTCTTTCATAACGG GGATGAAAATGACTGAGGCTTCACATTT GCACAGTACGATC	p000988	D	--
<u>229</u>	IM000847	AAGCCATCTGGGTCTCAAGTTGCTAAAA CTTAATAACTCCCTCCCTGTGTTTGTCTT TTATCTAATGGTAAAATATGACCTAATGA AATAGGTTCCCTAAGGCTTTCATATAAGGC ATGATGTTGAAGGATGGAGGACAGAGTG GGATGGAAAATCAGAGCCTGCACAGAAA ACCACAAGCAGCTAACAAAAGTCCACAA CCAAAGCCTGTGCCTGAAATGTCACCTA CAATGCAGTGGACTATTCATATGCCAGC CTGGTCCTCATGCGATC	p000991	D	--
<u>230</u>	IM000848	ACCAAGAACAGAGCCCCAACTAATAGG ATGGTTTGTTGCACGTGTACATGTGTATG CATGCGTGCATATACGTGTGTGTGTGTG TCTGTGTGTGTACACCCACACGTGTGCA TGTGTGTTGTGTGTTTTTAAAGCAAACCT CAGTGTGTCATACATACTCTCCTATACTT CCCCTCCCTTGTTCCATATGAGGGTGCC TTCTTATCTCACAGGGTTGTTTTGTTTTT TTCTATAACAGAATGCCGCTGATGCTCTT TTTTCTATATGAACCCTACATTTAATACTT ATCCATAAGCAAAGGAACAGTATCTTATC TTGCGGATC	p000992	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>231</u>	IM000849	CTGGGGGCTCTGCTACGCGTCAAACGC CTGGAGAACCCCTCGCCCCAGGCGCCG GCACGCCGCCTCCTGCCTCCCTGAGCG CTGCTGCATCCTGCACGCCCTGGAACCC AGGAGCGCCCCAGCGACCCTGACTCCC TGCCAGCACGTCCAAGGCTGCTTACCCC AGCAACCTCCCATCCCCTGAGCCCTCAG TAAATGCCATCTGTAGCAGCTGTTTGTCT GAGCGCCCTGTACTAGGGGGCCGGTGG GCTGGGTGACAATGATAATGGAATAGTG GCTGTCCTACTGAGGACAGCACAGTACT GTTTGGGACCTGTACTGGTAAGGAATAC ATGCCTGCTTCCTCTGGACTTTGCGGGT CTCACCGGGTGCCTGGGCTACCCCTTCTA GGCTTCACTGAGGCGGGTTCCTGGGA GGCTCTGAGGTTACTTTCAGCGTCTGCC AGGGGTCCACAGCACTTAGCCAAGGGG CTATGGATTCACTCGTGGTCTGCCAGGA CCAGGCTTGTTGTGAGGGCCCCAGGTG GATC	p000993	A	Saas
<u>232</u>	IM000850	GTGTTTCTTTTCTTTCTTTTCTTTTCT TTTCTTTTCTTTTCTTTTTTTTAAATCTAA GTAAGGTGCAACAATGTAATTCGAAGGG GCAGTGTCTTCCCTCCTGTAGTCTCTG CTTAATTCCTGAAGTTTGCCAAACCAGGA GTTAGGAAAAGTTGGAAACCTGCAGAGA GAGCGTTTGAGAGGTTTGAGATGTTATA CGAGAGGGTTTGGCAATGTGTGGAGTAC AGGTAACCTTGCAGTTATTGTTTTCTTGGC CCTCTATCTTCATCCTTTGTGCTTGCTAT TTACCTTGCTGTGCGATC	p000994	R	--
<u>233</u>	IM000851	GATCCTTGAGTCTGTACTTAGCCTGAGA GCGCTATAAACTATATACAAAGTACCGA CTAGAACTCCACACACATTTGTTGACTG ACTTAATGTGTAGCCCTGCAATGGTTGA CAGTTGGGGGTCAGGGGGCTCTTGCAC TGAGGGTAGTGTATAGCCTAAAGAGATA ATCAAGATGATAAGTACATCCACACTAG GACAGGAGCTTTAACAAGAGCTTTTAGT GAAGGGAACCTTCTGGGAGCCTCAAGGA AGGCATAT	p000995	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>234</u>	IM000852	AGCAACACCTCATGTGGGAATTCATACA TTGTAGGTAATCAGTCTACTAGCTGAACT ATATCTCCAACCCAGGAGGTCAGGTTTG TTTGTTTGTTTAAACAATCTAGTTTTGAAAC AGTCATATCCTAGGCTGGCCTCAAGTTA TGTAGTCAAAGATGGCCTTAAAGATGA CTCTTGGTTATTTTCCAAGTGCTGGGATT ATAGATATGCACACCACCACACCTCATTT GTCTCGGGGCTGGACTCAAATCCAGAGC TTCATGCATGTGAGGCAAGCACTGTACC AACTCGACTTTTGCATACTCCATTGAAAG TCATTTTATAACAGGATC	p000996	D	--
<u>235</u>	IM000853	CTACTTATCTATCATCTATATGTCTATCAT CTATCTATCTATCTATCTATCTATCTATCT ATCTATCTATCATCTATCATCTATCATCTA TCATCAATCATCTATCTAGCATCTATCTT CCAGAGCTCATGTTGTGGCTTGGGCTTC TCATTTCAACATCATCGAAGGTAGTTGCA TTTTTCTATTGGCTTCTTAGAAGCAGGA GGCAGATGAAACAACTTGCTAACCCTTT CCTGGTCTTTTGTGTTGTTGGTGGTGG TGGTGGTGATGGTGGTGCTGGTGGTGG TGGTTGATGTGCACAGGAGACCTGTCCG GTATGGAGATATGGAGAGCGTCTACGTC CTCATGGGATC	p000997	R	--
<u>236</u>	IM000854	GTGGGACGCGGAGGGTGGAGATGAATT GAGAAGCAGTTGTCGATTTCTCCTTCTT CCAAACATCAAAGGCAGCGGTGGATGAC AAACTGAAGGACAGAGGGTTTGATGATG CAAGAGGAGCCAGCAGCAACCAAGGCC AGCCTCTTGCGGGTGTGGGCAGGGCCT TCTTTACAATGAGTTCACACACACACACA CACACACAGAGAGAGAGAGAGAGAGAGAG AGAGAGAGAGAGAGAGAGAGAGAGAGAGA GAGACTGCTCTTTCAGAACAGCCCTAGG AGGTTAGCTTCAGACTAAGACAGGAGAC AGAGAGTCCTTGATTTTGCCAAGGTTGC ACAGCTGGGGAGAAACCCAGCTATGGCT TCACCTTGGCCCTTGTTAGGACTCCTTC CTAGTCCGGTTGCAGTCTCCTGGATC	p000998	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>237</u>	IM000855	GTATTAGAGGCCAGGCCATTGAGAAGAT GTGGCAAGATTGTCATGTGGAAAATATTT GAAACCATTCTAACCTAGTCATTCCATCA TCAATAATAATAATAATAATAACTACTA AAATGAAAAAACCTAGATATTTTGAGACT GTACTGCTGTATTTTAAGAAATACACGGA AATTTAGCACTGAAATTTAGTGCTAGTTT TAAGAATACTTTGTACCGTTACTTGGACC CACAATTGCTTAGAGCAAGGGATC	p000999	C	--
<u>238</u>	IM000856	GATCCTGAGACAGTACAGGAAGTAAAGAA GCCCTGGGCAATTTGCAGTGTGCACACC CAGCCTGAATTTGCCTGGTTCTCACCAG CCTACCAATAGAGCATTGTAGTGGCAGG GATGTCTGCTGGTGTCTCGCAGACAAC TTTGAGGTCCTGCTTCTCCAGAAGTGTG CAGCTGGCAATTAGCAGCCTGGTCTTTT CCTGTCCCAAGACCAGTGCTTCCACCA ACCTGGTCTCTTCCACAGCCCAGCCCT TTCTCTTCTCTTTGACACCCACTTCCTC TAAATGGTGGTCACATGCTTTGTCTCTTG AAAAAAGTTGTATGAGTCAGGGTATTTT CAACGCCGGGACAGAAAAATTGACTCAA CCTGGCTTTTTCAATTAACCACTAATGGG TTTCACTTACAGTCCTGACAAATACCAGG CACAATTCATCCAGGACAATAGTGAAGA ATTTTCATCTCTTCCCCCAAGCCAGTCA GTCTGGTTTTAATATGCACGGTGGATAG CCCATAGCATGCAATGAACTGTGAGCAC CCCTCTGGGAGTCAGCAGAGACACACAC ACAGGCACCCATACCACACACTGTGCTT TGATCA	p001000	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>239</u>	IM000857	GATCAAAACAATATTCAAATAATGACATC AGTCAAAGTATGATTTGATGGCCATCACT CATGTCAATAGGCAACACATAAGCCTGA GAGTAAGTTAAGGAGAAATTCAGCAATA AACAAATTGACATACTATGTCCACTATGA GTAAACCTGCCTCTCTTAAACGTTTTA CTGTACTCCATGGCTCTCCCCCAATGTG CGTTCGTGAGAGTCCCCACCCCTGTGAC TCCATCTGTGTGTGGGTTCAAGGAGAGAC TCCTGTGTGTATTCAAAGAGCCCCCA TGTGTGTACACACAAGAGACCCAGTGTG TGTACATGAGAGGCCCCACCCCATGTGT GTTTCATGAGAGACCCAACCCCTGTGCGT GTACATGACTCTCCCCATGTGTGTTTATA AGAGACTTGTGTGTATGGGAGACTCCAC CCTGTGTGTGTACATGAGAGACTCCTGC CTCTCCTGTGTATATGGAATACCTTCAGA GTATCAAATATTTTCACCCACTGAGCCAT CTTAGAACTTCTCTCCCTT	p001001	C	--
<u>240</u>	IM000858	ATACATATGTACACACACACTCACAAACA CACATATATACACATACATACTCAC ACATATATATACACACTAGTACACACATA CGCAAATACACACATGCATATACACGTA CTCACACATACATACCCATACTCACACAA ACACATATATACACACATACTCACATATA CATTACATACACACACATATATACAT ACACACACTTGCATACACACAGCACACA CTCACACACAGAGACACACAGACACACA GACACACACACAGAGGAACCCAAAGGAT TGGAAGAATAATTTCTGTGCTCAGTGG GAAAGTTTACCAGAAAGACAAGTGGTCA TGTGGGATGATC	p001005	C	--
<u>241</u>	IM000859	GATCAGGGACCCTGTACCCTCCCCCGTG CAGCCTGTGATTC	p001006	C	--
<u>242</u>	IM000860	GGACTGTAACCAACTCGGAGAGGAAAG GGCTTATTTTATTTTAGTCTTTACAGTCC ATCATTGACGGAGGTTAAAGCAGGACGC TGCTTACTGACTTAGCTCCCCGTTGCTTT ATCAGCTACTTTCTTAATACAACGCCACC CCCGCGGCCGCCACCTCCCTAGGCAAG ACCCACAGGTCAATCCAACAGAGAGGAT TCCTCAAGTGACACTCCTATGTCAACGC TATCAATGGCAAAGGTATATTGAGCTAAG AATTGATC	p001007	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>243</u>	IM000861	GATCTCAGGCTGCCCCGTGGGCGGGGCT GACGGAGGGAAGCAGACTAGGCCTCTA CCATATCCGTGGGAGGGACTTCCAAGGA CCGAGACTGAAGAAACAGCGCGAAACA GGAGACACTGGGAGGAGAGGCGGAGAC CGACACTTAGTAG	p001009	B	Mm.7675 3
<u>244</u>	IM000862	AGAGAAAAGACTATCTTGACCTTTGGATA TGCGGGTGCAAAAATGAGAAGACCACAG TGCAGCTGTGTGCCCTGCACGGGGCAG CGAGAGGAGAAAAGAAGCATTTTACATGA AGCACAGAACACGCCTGACAGTTCTCAA CAGCAGCACGTGAGACCACCGCAGCAC TGCTCGTTTTTCTCAGCAGACCCCCAGG AAGCACCAACCCAGGATGGACATGTAGG GGTGCATCCGAGAGAATCAAAATCACAC AGGGGCCATCCTTTTGGTTCGGCATGAA TGATGGGGGCCGCTGCACTGGCCTCC ACCTTCTATGTTGTTCTTCTTGTATCA ATGTTTCAAAAAAATCCTTGGGCTCACA ACTGCCTAATGACATCTTCAGGAGTCAA GTCAAGAAAGAGAAAAGTAGCCGACCTG GCACGTGGTAGATAAGACTCAAGGGTGC AATAAGCAGATGAACTGGCTTAGTTGGG CTTTCTATTGCTGTGATAAAACACCATGA CCAAAGCAACTGGGGCGGGGGCGGG GGGTGTCATCTTACACTTCATATCACAG TCTATCACTGAGGAAGTCAGGGCAGGAT TCAGGCAGGAACC	p001011	R	--
<u>245</u>	IM000863	GATCGGCCAACACAGGATAGATACCACA CAGGATAGGAGGTACAGTGTCTGGAAGA TTATTATCGAGCCCCTGAACGTAGTAGA AGCTGGCTGTCGTTCCAGTGCAAGCTGA GCAGATGGTCC	p001013	D	--
<u>246</u>	IM000864	GATCCACATGAAAGCCAAGCTGCACATT TGCTTCATATGTATGGAGAGGCCTAGGT CTAGCCCATGTATGTTCTTTGGTTGGTG GTTCAGACTCTAAGAGTCCCAAGGGTCC AGGTTAGTTGACTTTGTTGGTCTTCCTGT GAAGTTCCTATTCCCTTTGGTGCCGTCA ATCCTTCCTCCTATTCTTCAATAAGAGCC CGCAAGCTCCATCCACTGTTTGCTTGTG GGTATCTGTAA	p001015	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>247</u>	IM000865	CCCTCAGCTACATAGTCAATTCCCATCTA GCCTGGGTATGCGAGATGGCAGTAAAGA CACTAGCTGCAAAGCCTTACTGCCTGAG TTTGATC	p001018	D	--
<u>248</u>	IM000866	GATCCAGTCACAGGAGAGCAACTGGGG GAGGGAGCAGGACAGAAGCACACCATA GCCCTTTCAGGGGGCCGGGGGCGAGG GGTGGACAAGAGAAGACAGATAATGACT CACAGGATGAAGAAGCCTCCCACAGCCC CTCCCTGAACTGGCCATCTGTTCTGGGG CCCCAGAGCAGGCGAGTACCGTGAAGC TTGGGGACTAGCAGCCGGACCACTGAA CAAGGTCAACCAGCCAGTTGTCCCACGA GGGGAGAAGCTACCATTGAACTGTCACT TTGGAAAGTAGCCAGAGCCCATCCCTGG TCACCACCCAAC	p001019	D	--
<u>249</u>	IM000867	GATCCCTAGAGCTGCTGGTCAGCTGGCC TGGCTGAAACTACTTCTGTGCAGTGAGA GACCCTGCCTCAAAACACAGATAATGGA GACAGATAAATGACATCGTCCGCTGTGT CTGCGTGTGTATATGTAACACAACACAC AGTATACACACATACACACCACACTCATA CCGTCACACATGCACTCTCAGTGCACTGT GCAACACAACACAGTGTACACACATACA TACACACCACACACATACACATACCACC ACACACGCGCACACACACACATAA	p001020	R	--
<u>250</u>	IM000868	GATCCTTGTGCATCACTGAGCCATCTCC CCAGCCTACAGTGTAAGTATTCTATACAT ATTAATTTAATCCTGCCGGGTGGTGGTG GCGCACGCCCTTAATCCCAGCACTCAGG AGGCAGAGGAAGGTAAATTTCTGAGTTT GAGGCCAGCCTGGTCTACAGAGTGAGTT CCAGGACAGCCAGAGCTACACAGAGAAA CCCTGTCTCAAAAAACCAAAAAACAAAA CAAAACAAAACAAAACAAAATCCTATGG AGTATTCTAAAAGTAAAACCGTATCATT GCACTGCCAAATAACAGAAAAGGAAGACC AAAGCAAA	p001021	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>251</u>	IM000869	GATCCTCTGAAAATGGAGTTACAGATGG TTGTGAGCTGCCATGTGAGTGCTGGGAA CTGAACTCGGGACCTTTGGAAGAGCTGC TGGTGCTCTTAACAGCTGAGGTGTCTCT CCAGCCCCTTTGGGTGTGTTTTGTTTTGT TTGTTTTGTTTTGCTTTTTCAAGACAGGG TTTCTCTGTGTAGCCCTGGCTGTCCTGG AACTCACTCTGTTAGACCAGGCTGGCCT CGAACTCAGAAATCTGCTTCCCAAGTGC TGGGATTAAAGCGTGC GCAACCACTGC C	p001022	R	--
<u>252</u>	IM000870	GATCCAATATATTCATATGGAGATACATG TATATACATAA	p001023	D	--
<u>253</u>	IM000871	GATCCAGGTCCTTTCCCCCTTATGGTCC TATACACCCTGGGTACTTAGAGGCTTT CAGCTCTGACTGGTGGTGTGGGAGAA GTGAGGGGTTACACATGTGACACAGGTC CTAAAAGCTGTCGCCATTGGCACATGAC CATCCTAAGTCTGTGGCAGAAGGCTGCT CAGAGCCTCTGTCCAGGAACAACCCAAC ACATTGCAGAAATAACTGTGCATCTGGG CAATGGGGCAACTACTACCTGTCCATCC AGATAGCTCTTCTAGAGGCATTGAAATA ACACGTAAAGTGGGGTGGTGATGAACAC ATATAATCTCAGCCCCTGGGAACCGGAG ACAGGGGAGTCACAAG	p001024	D	--
<u>254</u>	IM000872	GTCACAGTACTTGCTCACTTGCCTCTCTC ATGGTTTACTCGCCCCCTCTTCTCGTAC CCCCCTTCTCCTACAATCCTCCTCGTCT ACTTTCATGCCGTATATGTCAAACACCGT CATATATAACAATGTATGCATGCAGCATT TCTTTTCTTTCCCATCAGCCTCCCTTGC TCCCCATCCTCCCGCCCTTCTCCTTCC TCCCAGGATC	p001026	D	--
<u>255</u>	IM000873	AGTTATGCTTGCAGACAGGAATGTAGCA TGGCTATCCTCTGAGAGGTTCCACCCAG CAGCTGACTCAGACAGATACAGATACCC ACAAGCAAACAGTGGATGGAGCTTGCGG GCTCTTATTGAAGAATAGGAGGAAGGAT TGACGGCACCAAAGGGAATAGGAACTTC ACAGGAAGACCAACAAAGTCAACTAACC TGGACCCTTGGGACTCTTAGAGTCTGAA CCACCAACCAAAGAACATACATGGGCTA GACCTAGGCCTCTCCATACATATGAAGC AAATGTGCAGCTTGGTTTTTCATGTGGATC	p001027	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>256</u>	IM000874	GATCGTGGTCTCTTCTCTTTTTCCCTCT ACTTCTTCTTCTTCTTCTTCTTCTTCT TCTTCTTCTACTGTCTTCTTCTTCTTCT TTCTTCTTCTTCTTCTTCTTCTTCTCTC TCTCTGTCTTTCTCTGTCTGTCTGTCT CTGNCTCTCTGTCTCTCTATCTCTGTC TTTCTCTGTCTCTGTCTCTGTCTCTCT TTCTCTGNGNCTCTCCCTGTCTGTCTGT CTCTCTCTTCTCTCTGTCTCTCTCTC TCTGNCTCTCTNTCTCTGNCTCTCTGNC CNCTCTGNCTCTGTCTCTGTCTNTGTNTN TCTCTCGCTCTCTNACACACACACAGAT GTACATGCAC	p001028	R	--
<u>257</u>	IM000875	GATCGGCGGTATCATATTTTATGTGTTTT ATTTCTGTGTGAGAAAGTTTAAAGGCCT CAGATTGGAAGTCTGGTTTGCATGGAAT GCATATGAGCTTTTTCATCTTATTGCCCA ACAGATTTAGTCTAAGAACCACCTCTATT ATATAGGGTATGATAAGTAATATAGGTAA GGGAATGCATCCCATTTGATAAGTGAAA GTTGAACACACATAGAGTTGGCTCACCC CGGGGTCTAGGCTCTAATCCCCTGGGG ATACCCAGGCCAACTAAACGCTATAGCA ACAGGCATTGGGGCATGAAGATACTTTT TGTTGTTTGTCTTGAATTTATATAGGGGC TTATATCTCATTACAATTAATCATGAGTTG CAGTCAATAAATCTTCATTGCTCAACATA TTTGTACCCTCAAATATTTTTTCTTTTTT TGTGTGATAT	p001029	C	--
<u>258</u>	IM000876	CTTGTAACACGATTATTTTAAAGATATA AATGGCTCTTTACTCTGTTTAAAAATTGT TTCTTTACCAGTTCTTCGTGTACATTGGT CTCCATTTACATGAAATAAAATATTTTGT TTAATGTTAGATTTTCAATACCAGCTGAG TGTTGATGTGTGCCTTTTGGACATATAT TTGTTGTAAAGTGGTCATTTGGGATC	p001031	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>259</u>	IM000877	GATCAGATTCAACTCCCGCATTCTAGC CCCAGCATCGTGGAAGGGCTACTGTGTC TTTTCAAGCACTATGGTGGATACACATAA TGCCAGCTTCCCTCATTACTGGTGATGT GAGCTGTTTGCCTAAGGTCCTTTCTGCC AGGCTTCTCTGCTGCCAAGGCTCTGAAT TTCCCTTTGTAGCTAATGCGTAGCCCTAT TGGCAGACTCTTCCCGTGGCTGACTTCT GCCTCCCGTCACACAGCAGTACCTTGTT TGTTCTCACCTTGATGTTTCTTATATGCA TTGATGATGGTGAACAGCCCAGCAAGTG CGCCTGTTTCTTCCCTTCTCCCACTTTT GTTCTCAGTTGTACATGGCAAGGAAAAC CAATTCCTTCTTTCATATTTCTCCAGAA AAAAAATCCTCTTTATAAGAGTTCACATC CTTGAGCACACATGATAGGAGCTGGTAG CCAG	p001032	D	--
<u>260</u>	IM000878	GATCATGATATTGTACTGCTGAAGACAAA CATATTTAAGATATAAGACTTGGAGAAAT CAAGTTGGTATTGACATTGGAGATTAATC TCTTTTGGCTAGCTTTTGTAGAGCTAGAA GTTGGTATGTAAGCTATAAGGAAGAGAA GTATTCATAAGACTTACCCAGTTGTCTCT CCTGTAAGCTAAGACCAGCCTAAGAAGC TAAAATTATCTTTAATGTAGAACCACAGA GAAAGAAATTGTGGTATGAATTTTGCTTG TTCGTGGACATTAACCATTAACCTCAATGA TAATCAAATGACAATACATAGAGACAAAG ATATGCATACTAGTAAATAGTGATAA	p001033	D	--
<u>261</u>	IM000879	GATCGTGCTAGAGAATGGTACACTTGGG TTATATTAAGAAATCTTGGTTGAGTGGTG GTGGCACCCCTCCTTTAATTCCAGCACTC AGGAGTCAAAGGCAGGCAGACATTTGAG TTTAAGGCCTGCCTGGTCTACAAAGTGA GTTCCAGGAAAGACAGGGCTATAAAGAG AAATCTTGTCTTGAAAAAACAAAAAAC AAAAAACGAAACAGTAACTGAAACCGAA AAAAAAAAGAAAGAAAGAGAGAAAGAAA GAAATCTTACAATGTGGGAGCTGGAGA GCTGGCTCAGTGGTTAAGAGCATTGGCT GCTCTTCCAGAAGACCCAGGTTCAATTT CTAGCACCCACATGGTGGGTCACACCTG CCTGTGGCTTCAGTTCTAGAGTTTCTGA CACTCACACACAAACATACATTCAAGT	p001034	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>262</u>	IM000880	GATCTTGTATTTCTTCTTGGCTTGTCTCC ATAGGAACAGGCAGCACAGCAGAGGTCT GGGAGATGGCTCCGAGGGTAAGGGACC AAGCAAGGTCACCTGCGCTCACTCCCTG GAACCCACACAGTGGACAAGAGAGAAAAG ACTCTATGGCCTCCACGTGCGTGCGTGC GTGCTGTGGTGTGCACGTGCCCCCTCCC CCAAATAAAGAAAACCTTAACGAAAAAAA TTAAAAGTAAAAAACAGCACTGCAGTAG CTCCAGGAATCAACTGGTCAATCAGTGT ATCACATTTGACTATCCGATGATGTTTT ATTTTACATGTATGCACGTGTTTGCATGT ATGTGGGTGCACATGTACAAACACATGT GCCAAGGCCAAAGGACAACCTTTGGGTGT CCTTTCTCAGGAGTCATCGACCTATTTT CTGAGACAGGGCCTCTCACTGGAATCTG ACTGGCCAGCAGCCTCCCAAGGATGCTC CCCAACCTCAGAAGGATGCGCCTGTCTC TGCCTCCAGCCCCGGGGGTACACTG GTGGACCACTGGGCTCTTTTACCTGGG TG	p001035	B	Mm.1388 34
<u>263</u>	IM000881	GATCTCTTCTTAAAATTACATTACAGTAG AAAATGTTTATGAGGCCGTTTTATCTCT AATATTATTTATTACCACTCTCCTACCCC CAGAGTCTTACAGGCATCAGGGAGTGGA CAAAGGCCGGCGGTACTGAATGGTGAT GTTATTTTTGAAATAATGAAAAG	p001036	D	--
<u>264</u>	IM000882	TACCTGTTGCTCCAACATGGTCAGAAAT CAGTTTGTTCATTTTAAGATACAATGA GAGTAACACCCTAAAGACTTCACATTTTA TGCATATTTGCTACTCTGTGAGCACATGA ACGCTTCTCCTTGGGCACGATC	p001066	D	--
<u>265</u>	IM000883	GATCGCAGATACTGCAGGTATGTAGTAA TGAAGTCTGTAAACATACAGAATGGAGA AGGCCAGAGAGGAAAGTGCAGGCATTG GGTAGTCAGTAGGTAAAATAT	p001067	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>266</u>	IM000884	GATCGCAGCTCTTCCTTGGTGCTTTTCC CCTCAGTTCAAGTGCTGTGGCGGGGAG GACTACAGAGACTGGAGCAAAAACCACT ACCATGACTGCAGCGCCCCCGGGCCCC TGGCCTGCGGGGTGCCCTACACCTGCT GCATCAGGAACACGGTAACTGCATGGGT GCTGGATGTGAGGGTCACCCAGTTTGCC AAACACTGCCCTCACTCTGCCCAAGTGG AGCAGGCAGTGGGAGTGGGTGGGACGT GGTGGCCGGGGCTGAGCTTGCCTTAGA CCAGGGGCCCTAGCAATGGGAGATGAG TGGGCAGCTTCCTCTGGGAGTGTGTCAG TGAGCGTGTGCGTGTGTGGGCCTGGCC CAGGCGCTTTGGTTGTAGTTACTTGGTT CTTACAACAGCTTTGGAGGGTCTCAATT GGGGTAGTGTTGCTTTAGCCACTTAGGG GGACTTGCCCAAGTTGGCAGGGCTCTT CCCAGCAACAGAGAGCCAGAGTGCCCG GCAGGTGCAGCAGGCTCTACCCAGTCA CTGGAGGCAGAGTACAGTGCAGGTGCT GTGAGCACTGGCAGCAGAGCCCTGGGC AGCGGCATGCGGTAATGTAAATG	p001069	B	Mm.2811 2
<u>267</u>	IM000885	CCATGTCAGGTGATTAACCTGTGAGTCT AACTTCCAGGAATGCAATGCCTCTGGCA TCTACAGGCATAAACATACTTGTGGCTTA CACTCAAACCTGACACACCAACACATATGT GCACGCGCACACACACACACACCAAATT AAAAATAAAATAACCCTTTTTAAAAAAAT ATAGAACCTATAGATAATTGCTTTACTGC ACTCACAAACATTTTAGGATC	p001070	D	--
<u>268</u>	IM000886	GGGGCACATAGTGAGTTCTAGGATAGCC AGGGTTATAGAAGCTATAGTGTGAGACC CTATCTCAAAAAACAAAACAAAACAAA AAACAAAAAAACCTAAGCCCGTGTGGT GGTGTGTCTCAGTCTGAGCGCTTGGAAG ACAGAGGGAGGTGCATCTCTGAGCTTGA GGCTAGCCTGGTCTACATAGAGAGCTCC AAACCAGTCAAAGTAACAAAATGAACTG TCTCAACAATGACAACAACAAACAAACAA GCACTAGAATAAAAAAGAAGCCAGCATGG TGTCATGTGCCCGTCATCCTACCACTTG GAAGGAGAGAAGCCAGTGCAGGAAAATT AGGGATC	p001072	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>269</u>	IM000887	GATCCCAGGCTTCCTGTAGGCTAGGCAA GCCCTCTCCCCACCCTGTCCTGGTAGAA TTCATCCCGAATGTCAGCATTCTTCAGT TAAAGGAATGTGCTCCCTCAGGCTCTCT CCCATGGTGCATTGCTTCAGCACGCAGG CAGACACTTGTCCAAGCTAGGCTCCCTG TCTCCCATCTGTAGGAAATGCTTGGTAT GAAGGCCCTGGTGGACCTGGCTAGATG GGCAGCGCCCACTGAAGGGCTGTGTCT GGAGCCTGGGCTGTAATTAGTGGTTTGA ACTGGGTGCTCTGGGGAGAGGCAAGTA AGAATTTGCTTTCTGTTTTAGAGCAGGA GGAGCTGGCGGCTGGCTGTGCCTTAGC CGGCTCCTCGAAGAGCATTTGAGGTGTT CGCCATCTTAATGGGTTAAGACTCTCCT GTGCTAATCTGGTGGGTTGCTTTTAGGC ACGGTGGTCCCACTGTGGTTGTGTGAAC AGTACCTTAATGCCAACACTTTGGAGGC CTAAGGTATCCCCATCTGCAGGAAGTGG GGTGCACA	p001075	D	--
<u>270</u>	IM000888	GATCCTCACACAAATTGAGTAGTACTAAC AAGAGTGTGATTCACATAGTCAATAAAG GTATAGGCCATCTGTGCCCTGGCTTGAC CTCCGCAGACCAGAAGCTAACAAAACCA AAACAGACTCAGTTTCTGCATGCTAACTT AACCATGATTTTCCAGACTATTTCTTTTAT CCTGTGAAAAATATATTAATCTCTATTCT GCAGAGTATCCCTTCTTTAAGAGAACAT GATTTCACTGTTTTTGACAATATGCCTAG ACACAGAAAAAATCATTTAGTTT	p001078	B	AA79335 6
<u>271</u>	IM000889	TTTTGAGTGCTCAGTGAAGTACTTAGGG CAGCCTAAGGAATACAGTGACCCACCAG GAAATGCCTTGTGTTTTGGCAGTCTGATA GCATCACTCACAGCTGTCGGTCGTGACT TCATTGGATC	p001079	A	<i>Edar</i>
<u>272</u>	IM000890	GATCCAGGGACAAAGAGCCCATCTCCT GTTCTTCGTAT	p001081	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
273	IM000891	ACTTTCAGGCAAGCTCTTTGCTCAGTGA ACCTGCTACCACACACAGACTCCTCCTC CCTGTTCCCGTCGTAAAAAAGTTTTAT TTGAGGTTTAGAGCAATGGCTCAGTGCT CAAGACTACTTGCTGTTCTTACAAAGGAC CTGGGGCTAGTTCCAACACCCACATGAT GGCTTACAATTCTCCAGTCTCAGGGGTT CCAGAACTCTTTTTCTGGCATTGAATGCA CATGATGCATATATAGACAAGCAGGCAC ACACACACACATAAAATAAAACAAATCTT TTGAATGTAATTTAAAAAGATTTATTAAT TTTAATTTTATGTGTATGAATGTTTTGCCT GCATGTATGTCTATGCACTGCATGTGTG CCTGGTGCTCAAGGTGTCTGATAGCCTG GTGCTGGGCTTGGTTCACCTCAACAGCTG GCCCTATGAAGGCCAGCCGTGAGGACA CCTATCCATGCTGACAGACACAGATGCT CAAATGAGACAGCCCCTTCTCTATGAAT GCCCTCTTGAGAATGAACAACCTCCCTG CAGCAGACCTCCTTCTGGATACCCTGCC CTTCCATACTTTCTGGGTGTCTAGTTCTC TTCC	p001082	R	--
274	IM000892	GATCACACGCTTCACCTAATTACAAATGA TTTCTTTAGAGGGGTCTGTATATAACAGA GATGATAAAATTCAACGGCAGCCCTCCA ACTGCATTGATATACAGGAAGTACTCATG AAATTGGAGACACTGATTATCTCTTTGTG TGGTGTCCACATATGTGCCATCATATCAT ATTATTATTATTACATGGCTAAAAATGG GGTGATAGGTTTCATGACCAGAACCAAA ATATTCCCCTGTAATTTACACAGGATTGA TGGTAAGAAATGAAAACAGTTTACATTTT TGATAATTTACTTACTTGACATAAAATGT GACTTTTCAATTCCTTGCAATTCCTTTTAC AGGTAAGGCTACGACAATAGATTCTCAG TTCTCCACCTCTCTCTATCTTGTCTACTC TATCAGCAGCAATAGCAACAGTTTTCCAT GGTCCCTTCCATCTGTAAAAGCAATAAAAA ATAACAAAGAAAACCATACAAACCATTAG AATATGAGTTGGTATTCACAACTCTCCTC TCAATACTTCATATTTAAAAATTACTAGA AATATTCATCAATAATATTTCAATTTGTTAG CTCTAGATAATGTTTCCAGG	p001083	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>275</u>	IM000893	GATCATGGTTATTTTTGTAGGGTTTATTT ATACATGTCTACATGAATTTATGTGCACC AGATGTGTGCAGGTGCCCATAGAGGCCT GCGAGGATGCCAGATACAGATAGTTATG AGCCACCTAATATAGATGTTGGGAATTG AACCCATGTACTCTGCAAGAGCAGCAAG TACTCTTAATACTGAGTCATCTGTTTAG CCCTCCTGTTGGGATTTAATGGTCAGTG TGAAATACTATGAAGATAGAAGGGTTTCC TAGACTCTGGTGTGTAGGGGTGGGGTAT CTGTGAGATGGGTAAGCTCTGTTGGCTT TCTAAGAAGGAGAATGAGCAGAAGGCAC ACATAGACATTCACTTTACACACATG CATGCCAAACACCACACATGCACACCAC ATACCACACGCGCCCTCCTGTTTCTTACT ATGTAATAATGTTCTTGTAACTTAGTA CTCTGCTAATGAAAAGGTCACCACTAACT AGATGCTAGCCTTCACTTTGGACCAGA ACTATGAGCCCAAATAAACCTCTTGCATT TATAATTTAGCCAGCATGTAGAACTGTGT CAATAACAATGGAATAGTGTTG	p001085	R	--
<u>276</u>	IM000894	GATCATCTGGCTAAAAATTTTATAATATGA CTCTTTAAATTCCTTAAGAATTCACAAGG ACCTTTATGTTGAAATTACTCATATGTAA GCTTACTGGAATGAGATGGCTCCCCAGT TGAAAACACCATTCTTAAATACTCAGAA AATAAGAACGAGGCCAGCCCGGTCTACA AAGTGAGTTCCAGGACAACCAGAGCTAT ACAGAGAAACCCTGTCTCAAAACAAAAA CAAAAACAAAAACCAAAAAAAAAACAAAA AAGAAAAACAAAAACAAAAACAAAAAGAA GTAGATATAAAGAAAGAATAGTGTTTGCT GGAAATAAATAGTAATATAAACTTAACAG CAGCCTGTCAATTGCAGGGTTTTTGCAC TTGCAGCTCAGAAAGAAGTGACCCTCCT CAGGAAGTAG	p001086	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>277</u>	IM000895	GTGGGTTGTGTGACTCAGAGAGCAAGCT TCTACCTCCACAGGCAAGGATGCCTGTG CACACAGAAATGAGATGAAGTCATATGT GGGGACTGGAGTTGCAGTGGCTCCCAG AAGGAGGTGTGCAGAGTTCAGGCTGGA GTCCAGATGAGGAACATCAAATAGAGAG GCCTTTGGAGGGAGTGGGTTCTCTTGAT AAGTAGGACTGCCACCCATATCAAGTAT AAGACTGCCAATCATACTGAATCTCAGG TTATTTCCCATGTAGCATTGGGAACATAT AGCATTGTGCACTGCTATAGCAAAGAA TCTGTGATGAGGTTGGGAGTGGAGGGG AACGCCTTTGGTCTAGAAAAAGAACCA AAGGTAGGCTGATC	p001087	D	--
<u>278</u>	IM000896	CCTGCCCTTGCCAGACCCGACCGCAGC TCATCGAGGAGGTACCCTCTAAAGTCGT CACCTTGAGGAGACAAGCTCTGTCATAG TGCTCGCAGCCCCGCGGCCCTGCGCC AGGTTGCGGACGCCATCTTCCCGCGCC GTCGCCGCCATCTCCTCCTCCTCCTCCT CCACCACCTCCCCCTCACCTGCCACTGA ACCTTTCCCCCAGCTTGAAGCCACGCC TTAAGGAAGCAGAGTCGGTCGGACACCC GCTCCTCCTCAGAGCAGCGGCCACCAG AGTCAGGAAGGGGGGTCCAATCACGT GATC	p001088	R	--
<u>279</u>	IM000897	GCTCAATTAGTTTATTTAAATCAAACAA AGCTAAAAGCCTGATGTGTCAGTTGCCT TCAGCAGAGCTGTTTGGGGCCCATTTGT AATGTTGTGAATTAAGTTCTGATGTAAGT AACCAAGCCACTCCCACACTCTTACTT GCAAGAGTTCCAGGCAGATGTTAAGGTC AACCCACCTGACTCTGATC	p001089	D	--
<u>280</u>	IM000898	GATCACAGTGTTTATCTCAGCAACAGAAA GCAAATGAGGACACACCTGGGTCTCACT GATATACTTGGTGATATGTGTAGTTATTA TGTCTCACAGTAATTGGACAAGGAAGAG AGTTCATTGTTTTAGAATGTTGTAAGTGG CATTGTTCTTCTCTCTCTTGTTCATAAA ATCTCACAATATCTACAGCTGTGAGGTC CAAGGGGCTCATTGGTGATACCCACTCT TTCTACTTTGTGTGACCAACCTCTTTTGG ATGTCAAGGGT	p001091	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>281</u>	IM000899	GATCAGTTGCTATTGCTTGATTGATTGCG AGACTTTCTTAACAAGAGTCTTTGTCTCC TCTCACTCCCTAGCTTCATCTTAGAACTT AAACCCACAGCCCAAATGAGTAGTTGTA TGTCATATGCCTCGGCCAAAGCACGACT GAAAGGAAAAGAAAGGCAGACACTGGA GTGCAGGAAGAAGACACAAGGCAAAGC CCAGAATTCAAAGTAGAAGCACAGATT GTTTTCTTTGTTT	p001092	C	--
<u>282</u>	IM000900	GTACCCTGCATCCCCGGTGTGGCCTTGG AGTCTGATGCCAGCACTACAGAGCCAAG CCATAATACAAACCAATAGAATTAACAA GAGCTCCATATGATC	p001093	D	--
<u>283</u>	IM000901	GATCACCTTCCTAGGATGAACGAAGAAG GATGGCTGGAGGTTAGGGACCCAAGGG ACTTCCCCCTAGAGCTGGCTGTGTACCC TAGGCATGTGTGACTGCAGCTGTACAAG CAGGGTATTCTGGGATTCACAGTCCTCA GGATAAGATGACACTACAGATTCTAAGC TTTATACCCAACATGGTGGAACCCCATG GTCACACTCTTTCACAGATGGTCACTCC CATTGCCCGAAGCCCAGCCTTTATCCAA G	p001094	C	--
<u>284</u>	IM000902	GATCAATAACAGCAAAAGAAAAAAGAA GTTTACTTTTCATGTAGCAATGTGGATAA TTCCCATCCAGAGAAACAAAACCAAGTTC CAG	p001095	C	--
<u>285</u>	IM000903	GATCAGGGAAGATGTCACCTCCAACCCA GCCTAGACATGGTGCTGTGACCA	p001096	D	--
<u>286</u>	IM000904	GATCAAGGAGCAACCCAATAGCTTCTAT TCCCCCCTACTAAAATATGACCCACTG ATGGATTCTGGGGATGCACAGATGTTCT CAGAAGTTACTGATGAACACACCATGCT CTAACAAATAGTATCAAACCCACAGTCAC AGATGGCCCTAGTTAAGCACAGTGCATC ACAAAGCAAAGCAAAGAGCCTTGACTGT GGGAAAGGTACTTGTGGTGAGGACTAGT GGGGTATGAAAGAAATTAGAGAGGATGA AGGTAGTGATATTCAGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTAAGACTATTAAGAACACCCTTTT TTAAAGAAAGGCTTTCTTGAGTGTACC	p001097	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>287</u>	IM000905	GGTTAATAAGCTAGATTATCGTGTATATA TAAAGTGTGTATGTATACGTTTGGGGATT GTACAGAATGCACAGCGTAGTATTCAGG AAAAAGGAGACTGGGAAATTAATGTATAA ATTAAAATCAGCTTTTAATTAGCTTAACA CACACATACGAAGGCCAAAAATGTAACGT TACTTTGATC	p001098	K	<i>Myc</i>
<u>288</u>	IM000906	GTGAACGACAGCAGAATCGGGTTGTACC TCAAAGCACTTACCTTTCCCAATACACCT GATC	p001099	D	--
<u>289</u>	IM000907	GATCAGTGACAATGTAGCTTTGCCTGGA AGGATACTTGAGTC	p001100	D	--
<u>290</u>	IM000908	GATCAGCAAAATGGGACATCGAAGTTGA ACCAAAGTCATAATAAAACATCCTGAGGT ACATAAACACTCTGTAATAGACTAATACA GTTCTCCAGGCACCAACAGAAACCTTG ACTACTTCCCTTGACTACTTCAGTCAAAT CTTCTGATAAAACCAGACCCAACTTGA AACGTCCATGTATACAATG	p001101	D	--
<u>291</u>	IM000909	GATCATCTGCTTCTACCCCCAATTAAGG ACGGACTAAGAACATAAAAAAGAATCCAG GCACCTAGGTTTGCAGAAATCTAAAGGT TGAGTTCCTTT	p001102	D	--
<u>292</u>	IM000910	GATCACAAGTTATAGTTGAATAACAAGTC CTGTGTGTGTCTATGTATCCGTATATCAT ATTTTCTTTATCTGTTACTCTATTTCATGA AACTAGGTGGATGTGTTAACTTGGCTATT ATGAGTTTTGCTGCTAT	p001103	D	--
<u>293</u>	IM000911	CTACAATGGTTCAGGCTTTGGAATATCAC TCTATAGGCTGTCTGCCGGCCACCACCC TTCAGACTGCCACTCACAGGTGCCCGTG AAGGCTGCCGAGAGGCAGTCCCCATCA GCCTGTCTCCTACACCCACACACTCTGT GTGGAGACCACAGGCGCCCAAAGGGTA TGCTAGTCTCTGCTCTACCGCGTACCCT CTCCTGAAGGCAGGCATTTTCAGAGATTC CAGTTTCACCAGGAAGCTCAGATC	p001104	C	--
<u>294</u>	IM000912	GATCTTTTCCCCCTTTGTAGTATCAGAGA GAAAAGCCATGGCATGCATGGCACATGC TAGGCAAACACTCAAGCATCCTACTCTG TGATGCAGTTTGAAACAAACTTTTTTTT CTTTTCTTTCTTTTTTCTTTTTTCTTTT TTTTTCTTTTCTTTTCTTTTTTTTTTTTT TGAGT	p001105	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>295</u>	IM000913	GATCTCTCCCCATCCTCCTGTTGCCTCTT GTCTGTCATACCTCTACTACTCCATCAGT TTGCTGCCTCTGAGTCCCTCTTCTTCCTC TCCTATCCCTCCTCCCATCTTCCTCATCT CCAGGTCTCTCCAGGTCTTCCTTCTTCC CTCTTTTCTTCCCCTTTTCCTCTTCCACT GTCTTGATTCCCTTCCTTCTCTGTTGG TCCCTTCCCTCGCACCTCTTTCCTCCTGT CCCTCCTTTTCATGTACCATATTTCTCTT CCTCTTTCTGTGTCTCCTCTTTCCTTCCT CCTTTACTTTCTTCTAACCTTCCTCTTTC TCCTCCTCCGGCAAGCCTTTGCTT	p001106	A	<i>Gata1</i>
<u>296</u>	IM000914	GGTTGTTCCAGTTAAATTGGCTCTCTACA GGAACATGGCTTAGTTCTCCCTTAGCCT TTCATGACCCTACACCTCAGACACTAGT CAAAGTCTAGCTTAATAAAGTGTTGAGGA TGTTGGTGGAGGGGGGAGATTGTTAAT ACAGATC	p001107	D	--
<u>297</u>	IM000915	GGACCACTTTAGTATGGGTCATATGTTCT AACTTTCTTTCATTTTCTAATTCTTCCAT CTGCATTGATTGTGCCAGTTATCATTAG TGACTTATTTAGTAACTTAAGGGAAAGT TGTCTATGCTCTACTTAGTGTGATTTAA CTTACTCTCCAGACATGGGAGTGCTTATT TTTGTTTGCCTTACCTCATCCAGGAGCTT GTAGATC	p001108	D	--
<u>298</u>	IM000916	GATCCGATTATGAAACCGGTTTTGAAC	p001109	D	--
<u>299</u>	IM000917	GATCTGTGGAATGCTATCCAGCTCTTCC AACAATAC	p001110	D	--
<u>300</u>	IM000918	TTAGTATCTGCATCTGACTCTTTCAGCTG TTCGTTAGGCCTTTCCGAGGGCAGCCAT GCTAGGCTCCTGTCTGCAAGCACACCAC AACATCAGTAACAGTCTCAGGGGTCTGA GCCTCCCCTTGAGCTAGATC	p001111	R	--
<u>301</u>	IM000919	GATCTGTGGTAATGATTCTGTAAATACAG ATAAACAACGTACACATGGGAATTGTTCC CTGTGTGAAAGTGTTTCATCATAAGGTGTT TTTATTTTATCTACAATATCTTTGGGTTTT TAG	p001112	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>302</u>	IM000920	ACTGCCACATTCCCTAACACCTCATCAAA GAAAACAACACCACAGGTCTCAGGCTGC CACTCTAGACCTCCGAGTTGACTCTGGC TCCTGCTCTCTGCAAGCAAACACGCATC CCTCAAGTCTTCATGCTGGTTCTCTCAAG TCTTCATGCTGGCTCTCTGTAGTTCTGTA AGCTTACCCTTTCAGTGGTGATTGGGG AGATC	p001113	D	--
<u>303</u>	IM000921	GATCTCCTGGCTTTGTAGATAAATGAAGA GAGTTCGTTACCAACTGAACTAAAGAGC GGCACAGGAAATTAACAAAAACAAACAA ACTGATAGTTAACTCAATTGAGTAAGTAT GGAGTTTTGGGACCAAGACATATTAGGC AAACAGACAGTTTAAGGCCTAG	p001114	D	--
<u>304</u>	IM000922	GTTCTGTACTTTATCATGTCTTACCCCT ACCTCCCTCCATTTAATCATCTTACTG GGATGTAATGCATTCTTTGTCCATTCCA GGATGCTATAACAAGATACCTTCAGCCT GTAAGCTATAGAACAGTGTGGTCCTCAA CCTTCCTAACTTTGTGACCCTATAATATA GATC	p001117	D	--
<u>305</u>	IM000923	CCANCGTGCCANACTCANAANGGAATTT TATTCATAGATTCTNTCANACTGCTGTCC CACATGTGTTCAAAANCAGGTAGGTCTT GTCANAT	p001119	D	--
<u>306</u>	IM000924	GATCTCATTGCACAGAAGAGTTAGAAGA AAGAAAGAAAAGCAGACTGGGAAAAATT TTTGCAGCGAGCATTTCAGAGATTGAACA TCTATCTAACTTATGCAAAATTCCTATCA AAAGAAAAAAAAGCTTCAACAGCTGGG TAAGTTAAATGTAAGTATAAGGCAACAC AAGGCAAAGTGTTGTTCTTTTGCTTGTT TCCGAGATGAGCTCAATTAATAATCAAT AGCGACAACAATTCTGAGCTGGACTAAC AAAGAGTAGAACAATACTACCCAACGCT TGTGGTTAGGTAACCTTACACAATATTTT CCTAATGCTATTCGGCAATAATTGTCAAG AAAA	p001121	D	--
<u>307</u>	IM000925	GATCTTTTCCTACAAGACTTCTGGGTGAC CTTGCCAAGCCCAGCCACTGGCTGTGGT ACCTCACCAGGACACTCGGTGGACATTA GGTAGTGCTCCCCAAGTGCTAGGTGACA GTTTATGCTTCAAAGTGACTCCTGCAC	p001122	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>308</u>	IM000926	GTGCTGACGCGCCCTTGCAATTTGGGAGA GCAGTCAAGCTATCTGTACCTTCACCGT AAGACTACATTGTCACTGCTGGCTTCCC TCCTGTGCAAGGGACGCATTTGGGTCAG ACTATGCATGAAACAGGACAACAAAGGT AGGGCCATTGGTAGATC	p001123	D	--
<u>309</u>	IM000927	GATCTCACTGAATATAAAAAGACATCAGT CCAAGGGTGGAAATTTAACCAAAATAATA CAATTGTTGTTG	p001124	D	--
<u>310</u>	IM000928	GATCCTCCAGGAAGTAGAGTTACAGACA ATGCCCGCCTTGTATT	p001125	D	--
<u>311</u>	IM000929	GTGGCAGTGACTGTCCGTGTGGGAAAC GTTTAGCAAGTCCGAGCGTGTTTCGATC	p001127	K	<i>Nmyc</i>
<u>312</u>	IM000930	CAGGAGAGTGTCTCAAAAAGCAGCAAAG CACCCAGCACCTTAGGGTGAAGGACCAC TTCTGGAATGTATCCTCCCAGTTGCAAAT GTACACTGTCTCATTCACTCCTGTGACAT ACTTTGTTTGTGAATGCTAATATCACATA GTTTCGATC	p001129	C	--
<u>313</u>	IM000931	CCAGCAGAGACCAAGCATCCAAAACATG AGCCCATTTCAAGGCTTCAACCATAGCAG CTCCCATCTCAATCCTGTTACCCCCCA CCCCACCCCCCGCTTCTCTATTTAAATCA CCTCTCAGTGACCAAAAAGATGCTCA TGGCAAATGGACTCTTGGCTCTCTTTTAC CTAATACTGAAGGTAACAAGATAATCAAC TGTTTCCTCTCCTTCCCGGGGACCTCAT CATAACAATTCTCCACATGAAATTATC ACCACGTCCAATACCCACATCCTCCCCG TCCTGTAGAGAAACCACATGCCTAGCAG CAGTGTTTCCCACCTCTGTGCTCCCTT CCACCTCGATC	p001131	D	--
<u>314</u>	IM000932	GATCGCTGTGGTTGGTGTCTGTGTATAT GCACTGTACATACTAACCAGGTACACAC ATAAATATTTAATATATAAAAAATAAAGTG CTTTCTAAGAGGCCCTTAGGCAGGGACG TTATAAAACATTTACAAAGCAGCAAAAC AAAATTGATACAATCAAAAAACAACACT ATAACCAACATAGGTGAAAACAGCCAAA CACATAATGTACAATCTGGTGTTCAGG ACAAACATCTGTATATACATGGTATATA CATACATACTTTTCACTCAATAA	p001132	B	Mm.3669 2

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>315</u>	IM000933	GATCGCTAAGTGTGCGCGGCCGCCGTC TGCAGAATGAATGGAGGGAATGAATGAG GGTGC GCGCGCCCCGAGGCCCGGCTTGC GTCAGCCATGCGTGCCCCGGCATGGACA CGGCCTGGCCTTCCTGGGAGGATGGGA CCGGATGCAGTTAGTCCAGGCGTTCAGC ATCCCAGGGCCCCTTCCTCTGTTGCGTGG TCTGAGTAATCTGTCTCGCAGAAGATAC CCT	p001133	B	Mm.1515 28
<u>316</u>	IM000934	GGAGGTCTCTGTAGGTGCTTAGACTCAC GTTACAGTCATTCCAGAGGAGGGAGCTG CAGCTGCTAGTTTCTGTGCACACCGATC	p001136	D	--
<u>317</u>	IM000935	GATCGGCTGTCAAGACTGGGAAGGGT CCTCCTAG	p001138	D	--
<u>318</u>	IM000936	AAGCAAGAGGTAATAAAATACATGTGGA TGGATGACTCAGGGGTTCAAGCATACA CCGATC	p001139	D	--
<u>319</u>	IM000937	GATCGGGGACCTTGCATAAAGGGGTCCA GGGCTCTCAGTCCTTGGGAAGG	p001140	B	AA70964 7
<u>320</u>	IM000938	GATCGTGATGACTTCATAACCATCACGT GTGAAAAGACTTAATGGCGCTGAATTCA CATGACACTTAAATGCACAAAGTAACAA ATTTTATGTCACATGTATTAACTACAGC TAAGTACATGGGGAAAAAGTTAGACTTA GAATAACTCATCCAGAGTCATATGGTAG	p001141	C	--
<u>321</u>	IM000939	GATCGAGGAGTAACCCAATAGCTCCTAT TCCCCCCTTACTAAATATGACCCACTGA TGGATTCTGGGGATGCACAGATGTTCTC AGAAGTTACTGATGAACACACCATGCTC TAACAAACAGTATCAAACCCACAGTCACA GATGGCCCTAGTTAAGCACAGTGCATCA CAAAGCAAAGCAAAGAGCCTTGACTGTG GGAAAGGTA CTGTGGTGAGGACTAGTG GGGTATGAAAGAAATTAGAGAGGATGAA GGTAGTGATATTCAGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTAAGACTATTAAAGAACACCCTTT TTTAAAGAAAGGCTTCTTGAGTGTACC	p001144	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>322</u>	IM000940	GATCGGGCCACATCTCAGACACTCCTAT AGCTACAGAGAGATACCGTTTCCTGTTAT CTTTGCAGACAACCTTTATCTGTTACTCAG AGAAAACCTCCAGGTGCCCTAAAGAAA CTGGGCCCTACATCACATACCCATACCA CACACATGCAACATGCAAAACATACACA CATACATAGACACACACACCACACGCAC ACAGACACATACAGACACACACACATAC TATACATACAGACACATATGCTACACACA TACAGACACACACAAGCACACATACTTC ACACACAGAGACACACACACCACACACA CACAC	p001149	R	--
<u>323</u>	IM000941	GCCTGCCTCTGCCTCTCGAGTGCTGGGA ATAAAGGCGTGCTAGAGCCTTCAC TTGG CTCTCTCTCTCTCTCTCTCTTTAACC TCCTTTTCCCTTAATGAGTTATTTATTTT TATTTTATGTGCATTTGTGTTTTGCCTGT ATCCGATC	p001151	R	--
<u>324</u>	IM000942	GCTTCAATATTCGAAAAGAATTAGTAAGA AAGGCTGTTCGATC	p001152	D	--
<u>325</u>	IM000943	CTACCAGGAAGTCAGGGGTTTCCAGGAA CCCACACTTGGCTTCCTCTGCACAGAGG GACCTCATACCAAGTGAGATGGTGATATG CTCCCTTGTTCTGAGCCTCAGTGGAAG CGACTTTCTATGGATACTCCCTCCCTCGT GCCTCTCCTTCTTTCCCTCTCTGCTCTCC CCCCCCCCCTCGCCCTCACGATC	p001154	D	--
<u>326</u>	IM000944	ATACACACCATCAGATATACCTCATTCTG ATATACCTACAGGTACACCAATCACACAC ACACATTTACTCACATGTACATGCACACA CCACATCGGTTAGAACCAAAGACCTCAC ACACACCCCTCACACATGTTTCATCTCCA TTATCAGTGCCGATC	p001155	D	--
<u>327</u>	IM000945	GATCGTCAGGTTATGAATGCCAT	p001156	C	--
<u>328</u>	IM000946	AGTTCTCAGAACCAGCTACTGTTTACACA GGGCCTCATGCAGCCTTGCTGTCCTCCA TTCTGCAAGCACAGGATACACACCCCTG AAGGCCAGATTGTCAGGTCAGCCCGATC	p001157	C	--
<u>329</u>	IM000947	CTTCAAACCGGTCCTGCGAGGAGTCCAC AACCTCTGCCTGCCGATC	p001158	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>330</u>	IM000948	GATCGAGGCCAGCCTGGTCTACAAAGTG AGTCCCAGGACAGCCAGGGCGATACAG AGAAACCCTGTCTCAAAACAAACAAACAA ACAAGATTCCATTGAGGAACACCCAGAT GGAGACATGGGTGTTCTCCATAGAAGGG TTAGGGGCTTCCACACCGTTGACAC	p001159	B	Mm.8136 6
<u>331</u>	IM000949	GATCGGTGTGCTTTCTGCAGTTTCAGCG AGGACTCTGGGCCCCAAATGTTTTAAAG CAGAAAATTGGTAACACTAGAGATATTGT CAAAATACGATTTCTCTGGTTCAGAAAT GGCGAGAGGGAGGGCTGGAAGGGTGG AGTGGGAAGGAATTGTCATCAAAGCATT GTTGATAC	p001160	B	AA40894 5
<u>332</u>	IM000950	CTGTCTCAGGCATGAAAACACTAAAAGA TGACCAATTTCAATAAAGATGACCTGAAT GTCTACTCAATTCACCATAAGGTCTAC AAGATGTAAATGGGCCGATC	p001161	D	--
<u>333</u>	IM000951	GATCGTGGAACAGAGCCTTGAATATAA TGAAGAAACAGAGGGCAGGCAGCAGCC GCAGCACAGCAGGGGCACTGTGAGCAG GCAGCAACAGGGGG	p001162	D	--
<u>334</u>	IM000952	CTCCCTACTACCTTCCCTTCCTGGACNT CCACTGAGATGAGGCAGGATAAAGGGTC AAAAGAGACCTGACCTTCTCTGCCAAAG CCAGGGATTTCTGGAAGAATAGAAATGG TTCTGGAATTCACAGATGCAGTGGTCTA GGATC	p001163	C	--
<u>335</u>	IM000953	GATCCATAGGTCTCTGCTTCCCCATTCA GGGCTGGAGTTATAGATATCTGTCTATC ACCCAGCTTTTATGTAGGTTCCAGG	p001164	D	--
<u>336</u>	IM000954	TATGTATCTACAAGCCAGAAGAGGGCAT TGGATC	p001166	D	--
<u>337</u>	IM000955	GATCCGAGTTCTCTCCGGCCACGTACCT TCACATCCCATGCACCCTGGTATGTAAG AAGAGCCCAGCTCAC	p001167	D	--
<u>338</u>	IM000956	TCCCATAATATTTCTCAGAAGGATC	p001168	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>339</u>	IM000957	TATAGTTCTGCCTGTGGAGTGTGAGCAG AAATGTGTATCGTTTCTGGGTCAGAGCTT TCAGGAAGTGAAGCATGACTGCTCTACAG TGTCTTTCTCCTTCTGCCTGCTGAAGCC CTAGGGGACAATAGAACCACAGGATGAA AGGACTCGGGATC	p001169	D	--
<u>340</u>	IM000958	GATCCAATGGCAGCTAGCAGAGTCAGAG AGCCCTCACTCCAGTTAACTAGGGGACC CACATGAAGTTCAAGCTACATATCTGCTA CAAATGTTTGAGGGACCTCCTAGCTCCA CGCCACATGCTCTTTGGTTGGTGGTTCA GTCTCTGTGAGCCCCACTGGGCTCAGGT TAGTTGACCTACAGTCTTCTTGTGGTATC CTTGACCCCTCTGACCCCAAGAGTTTAAC AATAGGCCTTCTGACTCTAGAAATCTACC TACATTTTTTCCACTTTAAATTCTCGGC TCACATAATACCAATGAAT	p001171	R	--
<u>341</u>	IM000959	GATCCATCTGCACAGTCTGTCACCGGGG TCCAGCAAGTAGCAGCCTTTCTGCTGCT GTCTGTGACACCCTCCAGGGAGGGAGA GCTTGTCTTCTGGCCTCCCAACAGGACC CTGCGTGACGATGCAGGGACAGCAATG ACAACTCATTCCAGACTCCAGGTCCCTG GAGGAGCCTCCCACAAGGGAAAGAGAC TACTTCACTGGTCCTGGGCCCTCTTTG CGCGCCCCGCCCCAGACTCAGCGTCT AGTGTTGCTGGGCTCCCCCT	p001172	K	<i>Pim1</i>
<u>342</u>	IM000960	AGGGTAACAGGCTTAGTTTGGGGCCTTT CTGTTACAGGAAAACCATGAAATGTCCT GAAGTGCTCAACAAACAGGGAATATAGA AAATCATAATGGTTCCTCCCTAGCACAAG GAAGCATGTTTAAAAATTGCAGCAAAATA AAAAAGAACAGATTCTTAAGATTGAGGG ATTTTACGGGGTGGTACTTTTTCTTTCTC TTATAAACATTTATTTACTTTTGTATTCA AGACAGGATC	p001173	D	--
<u>343</u>	IM000961	GATCCAGCTGTTTGCTAACATACGTAAA GGTATGGATGCTGAGAGAGTATCTATCG AAAGCGAAGGCACCCTCCCCAAATTCAA GAAAGCAGCTGTTTCTAGAACCAAAGAC ACCAACCGCCGCCGCCGCCACCACCACC CGCGAGCGCCCGGACCCTGTTACAGAG TGTC	p001174	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>344</u>	IM000962	GATCCTGAAATTATCACATTTGAATCAAA TCATGCCCTGCCGAGGATAAATAACCCA AACGACCGAGAAAACCGAGAAAAAGAAC ATTACTGACCATCCTTC	p001175	D	--
<u>345</u>	IM000963	GATCCAGTCCAGAGCAATGTTACGTCT GTGATGGTAT	p001176	D	--
<u>346</u>	IM000964	AAAGGTGCTCTCAATACTTAACAATCCAT AAGCTTGTGCTCTCTTAGTCGTAAAGGT GGGGTCCATCAAAATCCCATGACACCAC AGCGAGACCAAACCTCTTTTCTCTTACTC CGAATCACCCATCCCATGTGGGAGACGA ATAAGAACACAACTACATCTTCAGTGAC ATAGAGTAGCATCTGCAACAGAGGAAGT GGATGGAGACCTTGTCTCTGGTCAAAGA CAAAGCATGTGACAGCTGAGCCTGGCAC TTCCTACTTGGGTACAGCTCAAACCCA CCTGAACCAACAGCAGAGCCCCACAGG GATGGGACTCACATGTTCCCTCTTGCC CTGGAGCTTCGTGCATGTTGTTAGAAGC TAACTGGCTAACACGCACGGGAACAGGC AATGTAGTTGGAGTATGAATCGAAGTCA CTGGGCATGGTCCTCAGTCAGCCAGGAT C	p001177	C	--
<u>347</u>	IM000965	CTAGACTAGTATGGCAGAACCTATCTTCT TCTAATCATTTAGATGAATACTCCACATG AGAGAGCCCTGAGAATATCTGTAAAAAG TAATCCAGGTTCTGTTACTTCTAGCTAAT CTTATCTAGGTAATAATAGATAAGGAATC GGGATTCACGAACACAAATACCTGTACA AAGCATGTTGTCTCACACGGGACGAACA CTGTTTCTGCTGTGCTTTATAACGCTGG GACATACAAAACCTAGACTCTGCCTAAGA AGTGTTTGGAAACATTTGGGTAAATTAT AGTCAGATAAAACAACAACCATGAGTAAA TCGAAGAATATAAACTAGGGATC	p001178	C	--
<u>348</u>	IM000966	TTTCCTGGACAATAATGTTTTCTTCATTAA ATTTACACTTAGAGCATTGTCTTAATCCA TGAATAATTCCCAGCTCCTAGCTCATTAC CTGTGACACAGCAGGGATTCATACATTT ATTGAATGAATGGATGAGTGAATGAATAA AAGAATGAGCATATCAAGAGGATC	p001179	D	--
<u>349</u>	IM000967	GATCCCTTCTGTCTTTGGTTATCTC	p001181	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>350</u>	IM000968	GATCCACCACTGAGCCACTTCTTCAGCC TGTGACTGTCATTCTTAATCATCCACACA GACTTCTCCTTGGCAGATTTTGCCCACC TCTTAAGACTTTCACAAAGGTTTTTCTT CTGCAGGGCACATGAGAAAACAACCTCTG TCATAAAGAAACCCAGGAAGAAAACCAG CAGAGGCAGGTGAGTTAAGCCTGTGGT GGACATTCTTCTGGGGATGACCAGATG GGAACAGTAATTCACAGAGGCAGAGGG GTCTGCAGTCACTCTGCATGCCACATGT GTAACCCTTAAGAAGTGAGGAATGCTCT CAACAGGAAAAACACAGCAGCAAATGCT ATGATACCAAAGCCACAACCTCCATGGGT CCCTGGAGCCTCTCGAACTAAGCTGCCA GCTAGGGAGCTAACACTAGCTTTGGATG AAACACAGCTCTGGTAGAGTT	p001182	C	--
<u>351</u>	IM000969	GCTGGGATTTGAACTCAGGGCCTTCAGA AGAGCAGTCTGCTCTTACCCGCTGAACC ATCTCACCAGCCCCCTCCGTTCTTCCTT TCTTCCTTCCTTTTTTTTTTCCACATTGTT TTCAGACTGCACCTTGTTAGTAGTCTAG GCTGGCTTCCAATTCCCAATGATTGAG CTATGGGTATACTCTTTCACCTACTTTG ATTTTTGTTTGTATTTGTTTTTTGTTT TTTTGAGACAGGGTTTCTCTGTATAGCCC TGGCTGTTCTGGAACCTCACTTTGTAGAC CAGGCTGGCCTTGAACCTCAGAAATCTGC CTGCCTCTGCCTTCAAAGTGCTGGGATC	p001183	R	--
<u>352</u>	IM000970	GCTTCATTTAATATACATCATTTACCAGA AACCACAGACATCTTTGTACCAACATATA GTAATATTAATCACAATAGCCATCACTCT TATGTAAGGATGAGAAGACTCCCAGCTA ATATGCTAATGTGTAGAAGATGCCAGAT GGATC	p001184	D	--
<u>353</u>	IM000971	GATCCCTGCTTCTGTAAATCCGCAACGA CAATTGTTATCTTCTCCTTTTCTTTCTTT ATTTGTTTTATTCTATTTTATTTTCAGAT GAAAA	p001185	C	--
<u>354</u>	IM000972	GATCCTCCTGCCTCTGCCTCCTTCAGCA AATCCTACCGGCGTGCGCCACCACTACC GGCGAAAAA	p001186	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>355</u>	IM000973	GATCCCCCTTTCTCTCTGTCTACGGCCT CTGTCCTGTGTTAGCTGTAGGCCTACTC TGTATGAACAGACCTCAGCGGAGGGGTT TGGACTTGGGCTTGTGTTTCTTAAGAGA ATGGGGCTTCCATGACTGTCCCTCTGTC CCTTTCATCCTAACCCTGCCTCCCGCTA ACAGGCAGCCTGTATGTTTCTTGCACTG TTCCTTCCTCCTGACGGTCTGAGTCGTTT CCCTCAGAGACTGTTGCTGCTGCTTCAG CTTTCTCTCAGCTTCTCTCAGGGCTTCC GCTCTGGAGTTTCTCCTGCTTCTCTGTTT ACTTTTCAAAGCTCAGCCTCCATCTTCTG CACCTGCGGAGTCATCACTGATTCCCAG CTGTGGCCTGTCACCCTTCCCTTCTTTT TTCCTCCTGTGCCACCACCATGCACCCT CCCCTTCTGTCTGTTGTGTTGCTCCTAACC TTTCTTCTCCCCATGCACCCTCCCCTTCT GTCTGTTGTGTTGCTCCTAACCTTCTTCT CCTCTCTGTGCTCTGCAGGTTTATAGGT CTCTGTATGATTTGTACCTGCATTTATTT GAACCTCCACTCTTCTCTTCCCTCTCTT ATC	p001187	D	--
<u>356</u>	IM000974	GATCCTGCAATACCTCTCCTGGGCATAT ATCTAGAAGATGTTTCAACTGGTAATAAG AACACATGCTCTACTATGTTCATAGCAGC CTTATTTATAATAGCCAGAAGCTGGAAAG AATCCAGATGTCCCTCAACAGAGGAATG GGTACAGAAAATGTGATACATTTACAA	p001188	R	--
<u>357</u>	IM000975	ATCTAAACTATAATAGTTGCAGGGCTAGT TCATTGTCAGGTGCGTGGCGAAAGAGTG CAAATCCCGGGGGTTCTTCTTTCAGAAT CAACGAGGCAATACACTTGAACATGTAT GTTTTTGTAACTGCGGGGCATCACCCG TCCTCCAGGATC	p001190	D	--
<u>358</u>	IM000976	GATCCCCCAGAAGTGATAGTTTAACAGT GAGGTGAATGCAAGCAATAAGCTACCTA AATCATTAAACTTCTATTTTATTAGCAT CTATTAGTTGCACACAGCAGTGATGGGT TTCATT	p001192	K	<i>Irf4</i>

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>359</u>	IM000977	GGACCTCTGTACAAATGTCGGGAGATAA GGGAAGAAAAAGACGACAGAGATAGCA GTCAGGATGTAATGTGTACTAGATGAGT GGTTCAAGCAATAGGATGGAAAGGGCTT AGCAGGAGAGATTTTTAAGGATGGAGGC AGTAGATTACATCTGGGAAATGTCAGTG GAACTGGATC	p001194	D	--
<u>360</u>	IM000978	GATCACCAGGCTGGGCAGGCCACCTAA GGAAGTGGCACGGGCACGGGCACTTCC CCAGAGCACCTCTGGGCACTCTGAGA GGGGCACAGATGTACTGCACTAGGCTG GGCCCGGAGGAG	p001196	D	--
<u>361</u>	IM000979	ATATAAATATCGAACGTCCTCTGGCTTG TAAATATCATGTAAACCTTCAAAGCGTTC GAAAGCGCAGGAAATCTGAGTCAACAGA ATAGTATGTAAGTTATTTTTATAGAACCT GCCTGAACTGCAAGGGAGGGGCGGGGC GTGGACCCAGGCCTGCCTGCCAATCTG CGCTGCCAGTGAACCTAAGCCTGATC	p001197	D	--
<u>362</u>	IM000980	GATCAAGTCCTGGTCAGTACCAAGTTAA AAAAAAACTATATAAAAGCTATATTAGG GGACAGCTGTGGCTTTTGTAGAAAAGAA GGTCCTGGTGCTATGACCTGCAGATGCC CATGTGGAAGTCTTCAGATGAAGACTTT CTCATGGAGTAAACATACTCTGTTGTTTG ACCATGTGGACTTGGTTCAAAATGCCCA TGGATGCTCCTTTGGGTACCAGGCTTCA GTGGGAGTCCCAAGCCCATGTCTTTATT TGAGCATGAGCAGTACTGATGCTTACCT AGTCTTATTCTTTCCTTGCCCCCTGCCTG GACCGTCTCTGGTTACAAGGATGCTGCA GTGGGAAGCGGTATGACCGTTACCTTTA TGGGACTGAGACCACTAAGGGGAGGC TGAGGAGGCTGCAGTGAAGTTATTGTTG GGACTGTGGGCTAAGATGGAAGATAACA TGTTAACAACTCAAGTGCGGAGGTCTC AGAAGTAAATTGCCTGGTTAGTA	p001200	D	--
<u>363</u>	IM000981	GATCAATTGGTAACCAAGCCTTGAACCTG AAGAGTCGTGAGGTGGGGGACTTTATAT	p001201	D	--
<u>364</u>	IM000982	GTATCTCCACCTGGCTCAATATAGGCT CTTTTCAAAGGCTAAATTAAGACCAAGGA CACAGAAGGGTAGCTCGCTGGGCAAAC GTGATCCCTGCTGATAGTGTAG	p001202	D	--
<u>365</u>	IM000983	CTCTCGTGTGGAGATATTAAAGGTGTGA ACCACTAAGCCCTGATC	p001203	A	<i>Scp2</i>

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>366</u>	IM000984	GATCAAGCAGAGGGGTAAAATAAGGGCA AGCTCAGTGTTAGACAAGCTCATAAGCC AAAGCTGTGAACCTCTCCAACGCCT	p001205	D	--
<u>367</u>	IM000985	GATCACTTCAACATCAAGAAGTTACCCA GCCCCGGAAGAAGTACATTTCCAGGAA GCAGTGTTTTCATTTTTTGAGTCTGCTCC CATCCCGTTTCTCTGCAGCTGGGTAAAC TTGAAGCTGGGCTAGCCTCTGGGTAGAA GGCAGCTAATGACAACTACCTTGCCTGT CCCACGGAGCCCGGACAGAACCTGAGA TAACACACCTAGCTTGCTGAGTAAAGGC AGGTTACTGTGTGAATGACTCTGAGCTG TTCCAGCTCTGCAGAGCAGGAAGTCTGA CTGTGGAGATAAGAGATAT	p001207	D	--
<u>368</u>	IM000986	GTCATGATTTGTAATCCCTGTCCAACCTC TCATTGCTTAGGTCAAATGGCTTAACCTC CTAGCCTACTTCAGTGTAAGTCATGC GTAATGATC	p001209	D	--
<u>369</u>	IM000987	GATCAGGCTGGCCTCAAACCTCAGAAATC CACCTGCCTCTGCCTCCTGAGTGCCGG GATTAAAGGCGTGCGCCACCACTGCCTG GCTGCTTTCTTTTTTTCTTTTCTTTGTG TGTGTGGGGTAGTGGTGGTGGTGGTGG TGTTCAACC	p001210	A	<i>Hsc70t</i>
<u>370</u>	IM000988	ATGTGTGTGTGTGGCATGTGTGTGCCAT TGTGTGTGTGTGAGTGAGTGTGTGTGTG TGTCTGTGTATGTTGTGGAACAGATTCCCT GTGTATGTTTCCTTCTTCACACATGTTTT CAGAAGTGAAACCAGGCTATGAAGACCG CCAGGCAGCTCTGCAAAGCAGTACTGAG AAGGTGGGACACTGCGGGGGTGAGAAC AGTATGCATGATC	p001212	R	--
<u>371</u>	IM000989	GATCACACTCCATGAAGCTTCTCTTCTGC AACAGGAAACAAATAGCAAGCAAAACCA CTGGTAATCATTATGTGGTGTCTAACAGA GAGCGGTGACAGGGGTGGAACACTGAA TGACATTTAAAGGAGCTGGAGATGTTG GTTTAAGGCGTGTGGGGGCAGCCTACA GCATGGAATTGGTCCATAA	p001213	D	--
<u>372</u>	IM000990	AACCATCATGGTAGCTTCTGCTTCTCTCC ACGAAGATGGTTGTTCCACAGTTGCCC TCTCTACAGAGTGGTCCTGTATTAAGTCA CAGGTGCCATCCTGGTGATC	p001214	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>373</u>	IM000991	GATCTAACCACCCGTTTCCTGCCCGGTC TTAGATAGACCTCTTGGCCCCACGCAC CTAGACAATGGAGTAGACAAGACTTCGA GGGGAAAGAGGCTTCCCAAGATGACCC AGCTCATTGGCTTGACTCCCAACGCCAC CCACTTACACAGTGAGTATCTCTGGTCTT TGCTGT	p001215	A	<i>Farp</i>
<u>374</u>	IM000992	GATCTATGTCATCTTCCAGGACTCAGAG TTAAGAGAGTTACCAAGTGAGAGCTCTC ATCACCTTCTGAAGCAGTTGAGAATTGG AACCCAGAAAGATGCACATGCACGGGCA CACACACACCCACGGGCACACACCCAC CCACCCATGCAGAGAGAGAGAGAGAG	p001216	D	--
<u>375</u>	IM000993	TAGGTTGTGCCTGGCCTGTGCAGGACAT GCCTATGGGGTCTTCATCCCTCTCACTT ACTCTAATGTTCACTACTGACAAGCACTA GTAAGAAAGTAGGTGCCTGTAAGAGACT GGAGCAGCCTGCTGCTGACTTCAGCACC TGGGAGGCCTCAGTAGCAAAGCTTAGG GTTAGCAATCCTTGGGGCTGTGGCTGGC TGAGCTCTGGGGTACCGTTTAAGAGGAA AGCTGGAGTCCAGGTTCTCCAGGCCCTG GGTGCATCCCACAACCTCTCTCTCTCTC CTTTACCACTCGCAGCCTTGGCTAAGGA TGAGGACCGGGACCTGGAGTTATCTGAG ATC	p001217	A	<i>Snn</i>
<u>376</u>	IM000994	GATCTCTCCCCATCCTCCTGTTGCCTCTT GTCTGTCATACCTCTACTACTCCATCAGT TTGCTGCCTCTGAGTCCCTCTTCTTCCTC TCCTATCCCTCCTCCCATCTTCCTCATCT CCAGGTCTCTCCAGGTCTTCCTTCTTCC CTCTTTTCTTCCCTTTTCTCTTTCCACT GTCTTGATTCCCTTCCTTCTCTGTTGG TCCCTTCCCTCGCACCTCTTTCCTCCTGT CCCTCCTTTTCATGTACCATATTTCTCTT CCTCTTTCTGTGTCTC	p001218	A	<i>Gata1</i>
<u>377</u>	IM000995	GATCTTAGATGGCCAAATGTTGTGAACG TTTCCTAGATGTGTCGTGAGCACTCAGG GTTGAGAGCCCTGGTTATTTAGCAAGTG AAGTGGATGTATACACAAGCAGAAGGCT GAAACTAGACCCCGGTCTCTAATCCTAT ATAAAAACCAACTCCAAATGGACAATAGA AATAAGTGCAAGACTAACTCCAGGGTCA CTGGAGGGATACAAAGGGAGATGC	p001219	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>378</u>	IM000996	GAATGAATATATATATGGGACTAAATGCC ATGCCATAACCAAGAGAACTTAAAGAAG AAAGTGTTTAGTTATGCTTACTCTTTCAA AGAGTCCAGCTGCCAAAGGGATGCTGTC AGGAGTAGCTGAGAGCATACATCTGGAC CCATTAACAAAGAAGGGATGCTTCCCCA GCAAGATC	p001220	D	--
<u>379</u>	IM000997	GGAGGAGGGGCACCTTCTCAGAGATC	p001221	D	--
<u>380</u>	IM000998	GATCTTAAAGCTAATAGGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGGTC AGTGGTAAAATTGTCTACCAAGCTCTAG GTTCACCCCTCACAGAGCCGGAGAGAAA AGGAGAAATCAACTCAAGTCAACCCAAA CAAAACAAAGGACTCAACA	p001222	R	--
<u>381</u>	IM000999	GATCTGTTCCCAAATCCTCAGTACTCTC TGGGAAATGGCTTCTGTATGTACACATG TTCTCTAGCTATGTAATAAAAGACCTCTC TTCCTTGGCAAACTTAACTCTACCTTAG AAACTCTGATGAGTACTAGAAAGATGA CATGTTCCACAAACGTCTTAAGTGATTCA GGGTTCACAAACAAAGAAGGAGATGCTAT ATTGTCTTTCATGACATAGCGTCTAAGTC CCATAGCATAACTTCTATAACACACAAGT GGGT	p001223	D	--
<u>382</u>	IM001000	ACACTAGCTTCGAAACTTCTTAGTTGTCT GTCCCTGAGCCCTTTGTGGTACTTCCTC CTCAGAGCCCAGCTCCAGCAGTCCCCTT AGCGGCTGTTTTAGCAACCACACCCTC TGA CTGTGGGTTTGCTCTGCAGTGGCTT TAAGGTTTGAATACGAAATGCCTTCCACA AACAGACACTACAGAATCTTAGGTGTCTG AGACAATGGGCATTTGAGAAGGAATTGG AACCTTCAGATC	p001224	D	--
<u>383</u>	IM001001	GATCTAAAGGGAAACCCTTGTCTTTTGA ATCTGAGCCAGCACAAATATTGTATTCCT TCAATACGTGGTGAATGTTGTATTAGCAA CAATAAATGGAAGCAGGGAATCTCTCAT CTCATGAGTGATATTTACAATGTCTGTCT GGAAACAAACGGCTAATCAAGTTAGTCA CTTACTGTTCTTTAGAAAACACAGTACTT TGAAATGCATACCTAGCAGAGAATATAAA GTATTTACTGTTGGACTAGACTGGGCCC CCGGGTGTGAGGG	p001225	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>384</u>	IM001002	GATCTATCTCATCCTGTTATAGCCGAAAA CATGATAGCAGGATTGGGCAACTCTCCA GTCCCTTTCTCTTGGGTAAAGTCTGAAA GCAAATCGCCCGGACCCATCTCCTGTCT CTGCAGCCTGTCCCAGTTGCCTCTGCCA CTCACTAACTTCACTCCTTAATTTAAAAA GCCAGCACATTTATTGACCGTCT	p001226	C	--
<u>385</u>	IM001003	GCATGTCTCCAGACTCTCAGCTGCTTCC TGTCTGCTCCTGCTGGATGCTTCATGAA GATGGAGTGAAGCAGTGGTCAGCTTGTC TGTCTCAGCTGTTCTATGTGCATGTGTG CACTTGCTGGAGCTTATGTGCACCACAA GCACGCAGGTGCACACAGAAGCCAGAG ATC	p001227	D	--
<u>386</u>	IM001004	GATCGAACACGCTCGGACTTGCTAAACG TTTCCACACGGACAGTCACTGCCAA	p001229	K	<i>Nmyc</i>
<u>387</u>	IM001005	GATCGTGAGTTCAAGACCAGCCTAAAAT ACACAGTGAGCCTCTGTCTTTAAGAAAC AAACAAACAACAACAGCAAAAACAAAAAT ATTGCTCAAGACCCAATGTTCTCGGAC TATTTATAGGAATCAGAGTTGCTGTTCTT CTCAGGGCATGCCAGTTAATTTGAAAGA CAAGGTGTAGAGGCAAAGGAAAAGTGAT TTTACTTGGATAACCACTCATGGAGCA GTCAGGGGAACTCTAGCCTCAAAGCTCT TGCAGAAGTTATAT	p001230	D	--
<u>388</u>	IM001006	GTAGAAGCTTTTTAGAAATACGTTTCTTA TCTATCTATCCATCTATCCACCCATTATC ATCTATTATCTATATTTAACATCTATCTAA GTATCTGTTTATCTATCTACCTGTCTATA CCTACCTATCTACCTACCTACCTATAGCG ATC	p001233	R	--
<u>389</u>	IM001007	GATCGTGCATGCATGGGTGTGTTTTGGG GAGAGGTTCTGT	p001235	D	--
<u>390</u>	IM001008	GTTACTATTCATCTGAGGTTCTCTTTTGT TGTATTTGAACAGGAGGAAGGAACCAGG AGCTCAAGGATGTAGCTGGAAATGCTAT AAAACCTGGGATGCCCTAGAGAATCACAC GGACAATCCTGCTAACCCATGGATTGTA CACTCCAATATACAAGATAACATGTTTGT GCAGGCATGCCACCATGATGTTTCGATC	p001239	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>391</u>	IM001009	GATCGACCGCAGATGAGGTCTATGCAGG AAAAACGATGTCTGGAATTTTATTTAAAT TGCTCAGCAACTCACTGCCACGTATACT TGGAGAGCCACTTAGGGAT	p001240	K	<i>Myc</i>
<u>392</u>	IM001010	CCAAGTATACGTGGCAGTGAGTTGCTGA GCAATTTTAATAAAAATTCCAGACATCGTT TTTCCTGCATAGACCTCATCTGCGGTCTG ATC	p001242	K	<i>Myc</i>
<u>393</u>	IM001011	GATCGTAGAGAGATGGACCCAAATATCA GCCAGAGAATTAGACCAGAAAATGGAAC CAAAGTACCTGTCAGTCCAAGGATGTAG TGGCACTAC	p001244	D	--
<u>394</u>	IM001012	GTCCCCAAATGTAAACAAAATATCAAAA GAAATTGGGCATGCCAGAATTTTGTTCTT CACATTAAGGGAATTCTGAAATTGAAATC TTGCTAAGGGAAGGGTGGCTTGAGAATA TTAACAGAATCCTAGGTTGAAGGAGCAG GAATAGAGGATC	p001246	D	--
<u>395</u>	IM001013	CAGCTAGCCCATGGAGCTGCTGGGACA CGAGGCCCGCAGGCTGAGCATAATGGGG AAGAGATGGCAGATTCATTCACCCACTT GAGGAGACCACAATTAGTCAGAGGCATG CTGGGCCTGGTCAGAGTGCTCAAATAAA CATTACAGGACCAAAGTAATAAGCATT GGTGTTACAGAGATAAATCCTTTAGCAG GGACACGGGACCCAGAAAACCGGAAG GACATCGTTCCCATCATGAGAACAAGGA CAGCAAACAGTCACTGAGGGTATACTAC TGACCAAGTTCCAACAGGGATGGTCAGAA GTTGAACGCTGGATATATCATGAGCTCT GACCTAAATATTCTGAGTATTCCCCATGT TTGAATGGACTGAATACTCACATTTTCTA AATGCTGAATACTGAATTTTCATAGCAAC CATCATAAGGCATGGTGGCAGAATAATA TCTCTCACTCAGAAAGCAAATATTCTAA GTTGGGGATC	p001247	D	--
<u>396</u>	IM001014	GATCCCGTGGGGACTGAGCCTGCAGCT CAGTGGTAAAGCAGATGTCTAACGTGGT ACAGGGTCCCAGATGAGATGACACAAGT ACCTGTCAGTACTCCGGGAACACTGGGT GGGACTTTTATATGTTTATTTGATTCTTA A	p001248	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>397</u>	IM001015	AGTCCATTGTGTACTGAGAGAGGAGTTA GGTTTAGAAAGCCTTCCTCAGATGTCCC TCAAAGAAGCTGCTACAACTGCCCTCAT CCCAAGTTGCCAAGGATC	p001249	D	--
<u>398</u>	IM001016	AGATTGCGTGAGTTCTGATGCATGCTGG CCATGATGTGAGGCAGGGGCAGTGGTT GGATTCGGAGTCAGAAAACTTTCCCGTC TACTGCCGTAATTCCCAGCTAAATTCCTA TCCTCGTTGTAGCTGTTGGTGAGGATC	p001250	D	--
<u>399</u>	IM001017	GATCCTTCCGAATCTGCCATTTATTGAAT ATTTAAACACACCTCACTGCAGACTAAA CACATTGCAAGCACTGGGAGCAGAGGT GGCTAGTGAGCACCCTCTAGATGGTCC TTC	p001253	D	--
<u>400</u>	IM001018	GATCCTCCTGCGTCTACCTTCGGGTGGG ATTGCAGGCATGCACCACCATGCTTGGC TTTGTGTGGTACTGGACATTGAACCCAG AACTCTTTGAGCACTAGGCAAGCACATC CTGAACACCAGTAAAACATTTTCAAAGAG AAAAGAAAATTTAAACATACACCTATCT ACATCCATTTCCACCATGTTAGTAAACCA GGGACATTTTGAAGTGTGGTCTTTATAAA AACACCCGGGTGCTTATCTCCACGCTC T	p001254	R	--
<u>401</u>	IM001019	CCAGCGGTGCTCACTACTGCATGTAACC AGCTCCAGGATC	p001255	D	--
<u>402</u>	IM001020	GTCTCAAAGAACAATAAAGAGGAA ATTAGTAACGAGTCCTGAGAGATAGAAG AGTATTCAGCCTGGGACCAGAGCTCTGT CTTACAGTCTTGCCATTCTGTGGGCCT GGGACACAGCATCCTTGGTCTTTAGAAT GCCATAGGCCTCCTGAGGGAGCCTTTTC TGTAGGCACTTCTCCACATTCTTGAT GGATGCGATTTATTCTGTGTCAGGGGAC TAGGGTGCTGGATGTGTGGTCAATGA CTGTTGTTCTGTCACTTGGGAATTTGGG ATAGGAGAATTCTGAGTGCAAGGCTAGT CTGCACTTGAACGTACATATCGGGTTTTA AGCCAGCCTCTGAGCTACCACAGTGAGA CTCTCTCTTAATAAATAAACATAAATA GTCTTAGTATGGAGAGGTTAGGGGATC	p001257	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>403</u>	IM001021	CGTTTTCTCGGAAAATGTGAAAAGAAG AAGCACGAGACGAAACCCCCTCGAGAAT GAGAAAATTAAATCTAGAACCCAAATGG CGTCCAACAAGAACATTAGCTCTTGAAAA TGAATATTGCGCCTGCGCAGCCACCGCC CGGCCAGCTGCTCAACTGCAGCTAGAG CCCGACCCCAAGCGATC	p001260	C	--
<u>404</u>	IM001022	GTGTCACATGTATGAACAGCATCACATG GTATGAATGGTATCATATGGTATGACGT GAATGTGTGCACCGGCACTGATC	p001262	D	--
<u>405</u>	IM001023	ATACCACCCACTCCCTTAAGAAATGATC	p001263	D	--
<u>406</u>	IM001024	GACTGATATTAGTAGGTTGTTCTCTAAGG GCCGTGAAATTTTATAGCTAGAAGTTCTTG CTTTCATTAACAGTGCCAAGTATGAGTTC CATCTCATGGGGTGGGTCTTGAATACAA TCAGAAGGTGGTGAGTTATCGCCATAAC ATCTGTGCCGCTATTGTACCACTGGACA TAGTTGCCAGGCAGGCCATTACTGTAGC TCTTAGGTCATTCCTGAAGCTCTCTGGG GTCTGTTAGGTGAGACTGATGATAACTC TTCTCTCCGTTAGTGTACACAGCACCTT TAGCACTATGAAAGCGAGGCAGTATTG ATC	p001264	D	--
<u>407</u>	IM001025	GTTCCGATGTTTGTATCTCGTTTGAATTA TCCATCAGTTGATTAAGTTGATGGTCATC TAGGCTGATTCCCCTACATGGCCATCTC AATATTGCTTCTTTAATAAGACCTGGACA ATTAACAGCACCAAGTTGACATGCCAACTT GGATTGGGGGAGGGGTCTTAAAGGGCC CCGCCCTTAGATGAAGAGCTATACGCAA TTAATGACTGTCAGAAAGGGAGAATGGC TTTCCCAGAGATGAACCCCCTAATGGAT TACCCAGTACCAAGTGATC	p001265	A	<i>Rad52</i>
<u>408</u>	IM001026	ATTCAACCTATGGGGCCGTTAGACCCCT GGTCTTGGGTGGGGTGGATATGTTATTC TTTTTTGCTGTGGTGGCAGCAATTTTGT TGCTTTCTTGTTTTTGATACAGTTTCTC GTCATGTATTCTGGTTGCCTGGAATTCA CTTCTATAGACCAGAATGGCCTCAAATTT ACAGTGAACCCCCTGCCTCTGGCTTCAG ATTACTGGAATTACAGGTTTGTGCTATCT CACTAGTTGGTGTGTGATC	p001266	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>409</u>	IM001027	GATCAAGTCCCCAGTTAAATGCTTTCTTT GATAGGTTGCCTTGGTGATGTCTCTTCAT AGTAATAGAAAAGCAACCTAAGACAAGA GGAGAGAGTGGGTTTAAGAACGAGGAG AGAGAGGAACTCAGAGGGTCCTGGAGG TCCCGGGAA	p001267	C	--
<u>410</u>	IM001028	CTCACACATACATTCATACATACACACAC ATATATACATACACACACTTGCATACACA CAGCACACACTCACACACAGAGACACAC AGACACACAGACACACACACAGAGGAAC CCAAAGGATTGGAAGAATAATTTCCCGT GCTCAGCGGGAAAGTTTACCAGAAAGAC AAGTGGTCATGTGGGATGATC	p001270	C	--
<u>411</u>	IM001029	GATCATCACCAGTGTAGTGTGGCTTTAA CGGTGCACGCCTTTAATCCTAGCACTTG GGAGGTGGAACAGGTAGGTGTGCTTAC TTCAGTGAGTGAATTCAGGCCAGGCAG GGATACAGAGTGAGAACCTGTTATCTAA ATAAATAAATAAA	p001271	C	--
<u>412</u>	IM001030	CACCCACGGCTTGCTTCTTTCTCTATGT GTAATTGAAGCACATACCCGGTGGGAGC CATGTAAAGCCTGTGTCCATGATC	p001272	D	--
<u>413</u>	IM001031	GATCATGTGTTAATGAAACTGTCAGGGG TTGGGTAAGATGGCTCAGTAGGTAAAGG CACTTGCCTCCTAGCCTGGAGACCTGAG GTTCTCCTGGGGCCACAGGGAAAAG GAGATAACCAGCTCTCTGTCCTCTGACC TCCTGGGCCCCCTCCCTCACAAACAAACA AACAAACACACACAAACGACCAGACC ATTTCCACAGTAGCTGTGGTGCGTTAC ACTGTAACGGGCACCATGTGAGGGTTTG GGCTTTATCACATCTCCGCTAGTCATACT TGGTGTTTCTGCGTCTTGCTTACAGTTG TTCTAATGGGTGGGCGGTGATATCGAAT TGTGGTTTTAGCATGTATTTCTGTGCTC TGCTAAGACCACTTACAATTACAG	p001274	R	--
<u>414</u>	IM001032	CCTTAACGCTCCCTTGATGTCCACTCCC GTTTTCTCTGCAGCGATTTATTGCTTAGT CTATCTATAAGGTGTATGCAAGCTGCAA GTCAAGTATTTCTTTGTAAGTTGAGCAAG TCTCCTAAGTATTATGCTTCATAACGTTG TGATATGCTTGAGCAAATTTGAGTCTATT TCATAATTAAGCCACTGTTCTGATAAAAG ACCCTAGAGTGCTATATCTGATC	p001277	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>415</u>	IM001033	AAAAGAGTGTGAGATGTCAGAACTGACT AGCTGGGCTGACACTGAGGAATGAAGGT TGGGGATATATGCACCTCCTGAAAACAG GAAGCCTTTTGTTGGTTGATC	p001279	D	--
<u>416</u>	IM001034	GATCAACCTTAGTACACAGCAGAGTGTT TTCTGGGAAGCTCATGGAGACCCACTTT TGTCATCCCATAGAGGTTACTACAAATCT GAGCATGAGAATAACTACTTGCTGTTTAA TACAAAGAACCATTAGCAGTCAATGCCC CAAGTTCTAAGGGCACAGACTTCATACG AGAAAAAAAAACAAAGCAAAACAAAACT ATCACATGCTACTATCTGTACTGGGGAAT GCATACAATTTGTAGGTAT	p001281	D	--
<u>417</u>	IM001035	GATCAGTAGAGAGCAGAGGGGTCTATGA GGGAGGTAGAGCAGCCTGGGAGGCCTG AGGAAGGAGGGACAAGGGCAGAGTCTT GGTCACTCTTTGGTCTAATTGCCTTCAGA AGGCTTGCAGACTCTGGTTTGGAGTTCC AGGTGGGTGGCTG	p001282	C	--
<u>418</u>	IM001036	CAAGTAGGGTTTGTGTGTGTGTGTGTGT GTGTAGCCAGTGTCTTTCTCAATCACTCT CCACCTTAATATTTTTTTTTTGAGACAGAA TCTCTCACTGAACCTGTATGCTGTCAATT TGTCATGGCTGACTGGCCAAGGAGCCC GAAGAATTTATCTCTATGCTCAATCCAAC CCCCAGATC	p001285	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>419</u>	IM001037	GATCACATGGACCGATTGCCGCGGGAC ATCGCACAGGAGCGTATGCACCACGATA TCGTGCGGCTTTTGGATGAGTACAACCT GGTGCGCAGCCCACAGCTGCATGGCAC TGCCCTGGGTGGCACACCCACTCTGTCT CCCACACTCTGCTCGCCCAATGGCTACC TGGGCAATCTCAAGTCCGCCACACAGGG CAAGAAGGCCCGCAAGCCCAGCACCAA AGGGCTGGCTTGTGGTAGCAAGGAAGC TAAGGACCTCAAGGCACGGAGGAAGAA GTCCAGGATGGCAAGGGCTGCCTGTT GGACAGCTCGAGCATGCTGTGCGCTGT GGACTCCCTCGAGTCACCCCATGGCTAC TTGTCAGATGTGGCCTCGCCACCCCTCC TCCCCTCCCCATTCCAGCAGTCTCCATC CATGCCTCTCAGCCACCTGCCTGGTATG CCTGACACTCACCTGGGCATCAGCCACT TGAATGTGGCAGCCAAGCCTGAGATGGC AGCACTGGCTGGAGGTAGCCGGTTGGC CTTTGAGCCACCCCCGCCACGCCTCTCC CACCTGCCTGTAGCCTCCAGTGCCAGCA CAGTGCTGAGTACCAATGGC	p001289	K	<i>Notch1</i>
<u>420</u>	IM001038	GATCTAACTCAGGCTGTTTCAGCTTGGCC AACAAGCTCAAATATCCATTCCGCTGTCA CATCGGGCCCCATGTGATGCTTTATATA CTAAATAGAACAAGCAAATTGATACTAGA TGGGACAGTCTGCTTACCCAGTTTGGTG TTTGGTGGGGGAGGTGAGACATATCCCA CAGTCCCAGAGCAACTGTCACTGCAGGG TCCCAGGGGAGGAGCCAGGTGTGAAGC TGGCAGTGTGTGAGGTACCCTGGGGAA AATGAATGGTTACT	p001292	D	--
<u>421</u>	IM001039	AGGCCTGGTAGTGACCAGCAAGTACTGA ACGCTCGCTCTATGCCAGACACAGACCC TCTTCTTCCTTCGTCTTATCCTATTATCCA TACTGAACAGACAAGGAAATGAAGGCTT AGATGAGTCACCCGACTTGCTGAGATC	p001293	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>422</u>	IM001040	AGTGGGGCCTGAAAATCACATCTGGGCA AACCCCTGAGGCCTGCCAAGTCCTCATCA GAGGGATGCCCTCTTCATCCCAGGTGCT TTCTGACTATAAAATAAGGTGAATACTAC CTCCCCTGAGGTTACACCTCCAGGGTTA AGCTGGTTAGAGAACCCAGGGACACACT GGGAAACAGCCCACAACAGCAGGAGCT GGAGCACTCACCCACGGATGTCCATGG GGTCCAGCTCCCTGCGCTGGCGCCAC CACTGGTACCAGGAAGCAGTGAAGAGGT GGCCCAACCCACTGTAGAGCGCTTGATT GGGTGCTTGCGCAGCTCTTCCTCGTGCG CATAGTACGGGAAGATC	p001297	K	<i>Notch1</i>
<u>423</u>	IM001041	AGTGGAACCAGATTCCTCCTACGCTTTG CACTCCACTTTTCGTTTTCTCTTCTGTACC ATTCTAATGGAGGCCAGAGTAGCAACTG TATAGACAAATCAAATCGTTTACTCTTCC AGTCTTGCCCCTTAACAGTCTTTCCTTTG TTCTTCCTCTTAGCCTCATTTTCTCCTTC TCAGATC	p001298	B	AI604147
<u>424</u>	IM001042	GATCTTCTGCTTCATCTGAGTAGGCTTAG ACTGGTTTGTATTATTATTATTACTTG TTGTTGTTGTTATTTTGGTGGGAGTAGTA GTAGCAGTAGGTGTGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGT ATGTATATGGAGGCCAGAGAACAGCTTC TAGCGGTTGCTTCTCTCCTTCCTTCCACT GTGGTCCAGGGAATAGAACTCAGGTCAT CAGGCTGGGCAGCTGTCACCTTTAATGC TCTGAGTTATCTCACCAACGTTAATAAAA GGCTTTTCAAACAGCAGTTTGGGCTGGG CCTGGTTGTGCAGACCTGGAATTGCAGC TTCTTAGGATGCTGAGGCAGGAGGACTG GAAGCTCAAGTTGTGTCGGGGAACTTA GTAAGTCCCTATTCTCGTCCCGCACGCC CCCAAAAAGCCAAGACCAAGACCAAGCA GTTTGGTACAGCAGAAAAAGCACGAGAG TCTCCTCCTCCTCCTGCTCCTCTTAATG ATGCAGAACCC	p001300	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>425</u>	IM001043	GATCTGTGCATTATTCTGTTGGAAATGTG ACAAGATTCTGTTGAGAATCTCATACTCT ATGAACTCTTAAAAAAAAAAGGTTTCTGC TGTTTTGAGACAAAATTACTTATAAAGGT TTATGATGTAGTTAAGGCCCTGAATGTCC CCCAAAGACATGTGTGTTGAGGGTTTGG TCTCCACTCCGTGGTCTTTTGGGAGGTG TTTTATGTTAGCTGGTGAGGCATAGTGG CAGGGGAGGAGAGTTGGGTCATAGTCC TTTTGAAGAGGCTATTCAGGCTCTGGTG CCTAA	p001303	D	--
<u>426</u>	IM001044	GATCTGACTGTGATAGGAGGGTCCTGGG GCCACCCTGACATAGGCCTGGTCTATGA ATGCTCTCATGGACTGGGCCTGTTTGTC A	p001305	D	--
<u>427</u>	IM001045	CTGCCTCTCTCCCTGGTCCCTCTCTGAG GTTCTGGACCCTCAAAGGCCCTTTCCC ACCCCAGCCTTCAGGCCTGTAACCCAGC CTCGGTTTCTCTCCATTGCCAAAGCAC AATGGCTGTTATAATTAACGGATTATCTC AGCGCGACAGCTGCGCCCCCTTTGAAAAT TAGGTTGAATAACAAGATC	p001306	C	--
<u>428</u>	IM001046	GATCTTGGACCACCACGTCAAGCCTCTT GTACATTTCTTTGAAAAACAAAGCTTGGT TCCCCCTAGTCACCACGGTGAAAAAAC CCAGGACAGTAAAGGTCCCAA	p001307	D	--
<u>429</u>	IM001047	TTAGTACCTCTGGTGGAATCACCATGCC TGACCTAAAGCTTTACTACAGAGCAATTG TGATAAAACTGCATGGTACTGGTATAGT GACAGACAAGTAGACCAATGGAATAGAA TTGAAGACCCAGAAATGAACCCACATAC CTATGGTCATCGATC	p001308	R	--
<u>430</u>	IM001048	GATCGCACCGATTGCCAGTATAGTACCT AGAGTGTCAAGTTGGCCTCTCAGGGAAG AGAGAACATGTATTAGGGTAAGACGCAA GCCCCAGTAAAAACATGTGAG	p001311	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>431</u>	IM001049	GATCGCTTCACCAAGTGTGAACTGTTGG TAGGGACAGAGCAGACCACAAGCCCCT CTTTGCATTTACATGGGGGCGTCCTAGT GTAGGTGGCTAGGGATGGTGGACAGGA GAGGAGGGAAGACAGTATCACATAAGAA CAATAGTGGAGGGCAGGGGAGGAAGCC TTCTCATGGCTGGGGTGAAGTCACTTCC GTAGCCAGAGCTGACTGAGAATATCACT GCTTTCCTAGTAAGGAAACACCGGAAGT CGGAAGATGATAAACGCGAAACTCACTA CATCATAGACACCATTTCTGTCTTCATCAA CAGAGAAATTTATAA	p001313	D	--
<u>432</u>	IM001050	GATCGTCCACTTCTGTGTTTGCTAGGCC CCGGCATAGTCTCACAGGAGAGAGCTAT ATCTGGGTCCCTTTCAGCAAAATCTTGCTA GTGTATGCAATGGTG	p001316	R	--
<u>433</u>	IM001051	AGGGTACAGCGAAGCTTGAAAAAGCAA GGAGTGCTCTGGGACCGGGAGTGATGG AGAAAGTCTGAAGCCCCTTGCACACCC CTACAATGGGTTTGCGCCAAGAGAGGCG CCGGCAACTCTACGCGGCGTGGGGCTC TCCCCAGCGCTCTAGTTCTACTGTGCT GAGCCACACTAGTTTCTCTCCCTAGACC TGAAGAGACCCCAGAAGTCTGAGAGTCC CTTTGGTTCTCCATCTCTCACCACCCCC CACTCTCGTGCTTTAACTCTGAGGAGGG CCACTCAAGTTCATTATAAGAACAAGG GCTTTGCTCTTAAAGGAGCCGCATACCG AAAGCGTTTGTGTGACTGAGGGTTCACA TGCACAGAGCTCCGCGTGTCTCGACATC CTCTCTCTCCGATC	p001317	D	--
<u>434</u>	IM001052	ATCTCAGGAACTCCTAGCAGCTTTAGTA CGCATCGTGCTGTTTCCAGCTGTCGGTA TTTTACACAGTTTTGAGCGATC	p001318	D	--
<u>435</u>	IM001053	CCTTCAGGATTACTTTGGATGATTCATTA GAGAATCTTGCTTTAGACTATAAAGCAC TTGTTGAACAAGGTTACAATGTAGCAAG CAACCTTGTTTTGGAATGTATTTTGCTAC ATTGTGCTCTTCCCTGGTCTGGTGCTTTT ATTCACATATTTTGCTCTTAATAGAAGTA GGGTTCAAGTGCTGGGGATTTCAATTTGCT GTTTTCTCCATTGACCTCTTGAGCTGAAG TTATTCTTATTAGAAAGTCAGGGTAGGCG ATC	p001319	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>436</u>	IM001054	CCAGCAGGCAGCGAGACGCATTTTCGC GTGGCGGTGGTGAGCTCTCGTTTCGAG GGGATGAGCCCCCTTGCAACGGCACCGG TTGGTCCACGAGGCACTGTCGGAGGAG CTGGCTGGACCGGTACATGCCCTGGCC ATCCAGGCGAAGACCCCCGCCCAGTGG AGAGAAAACCCACAGTTGGACATTAGTC CCCCCTGCCTAGGTGGGAGCAAGAAAA CTCGAGGGACCTCTTAATAAATACCTGG ATTGGGAGAACGATC	p001321	B	Mm.1045 31
<u>437</u>	IM001055	GTTTTTCCTGCATAGACCTCATCTGCGGT CGATC	p001322	K	<i>Myc</i>
<u>438</u>	IM001056	AACTAGGAAAGGGTATAGCATTTGAAAT GTAAATAAAGAAAATATCTAATTTAAAAA CAAAAAAGAAAGACAAAGGAAAATTAAAA AAAAAAAAAAAAAGAAACAAAAGCCACTG CAGGACTGCCCAACAGTCTACTGAAAC TGTGAGCCTTATTCTAGATGAGCCTCT GATGCCTCCACTTACAAGCTACCTTCACT CCTCCATCTATCTCCTTTTGTATGTCCC GCGATC	p001324	R	--
<u>439</u>	IM001057	GATCGGACTCGAAGAGCAGAAGAAACAA AACTCAAAGCAGGGATTAGGTCAAATT AAAAAGGGTTTGACACAAAAGGAAACC ATCCGAAGAGACAACCTACAAAGTGAGA GAAACTTGTTTTGAAC	p001325	D	--
<u>440</u>	IM001058	GTCTGAGAAATTGTCTTTAATGTAGTGAC TGTGGAGCCTTGACAGGGATACCCACGAT GGGGGTGTCAATTCATATGTCACTGCACC TGGAAGACCGATC	p001326	D	--
<u>441</u>	IM001059	GATCGCACAGCCTGCTTTCTCAACAGTA GGTAGGACCAACAGCCTAGGTGGCACC ACCCACAGTGAGCTGGGCCTTCCACATC AATCATCAATCAAGAAAAATAGCACAAAA CCCTTTCCCGAAGGCCAATCTGCTGGAG GCATTTTCTCAGTTGAGATTCCCTCTTCC CAAATGACTGCATAAACTTGTGTCAATGT TGACATGAAACTAGCCAGCACAGGGTGT	p001327	K	<i>Pvt1</i>
<u>442</u>	IM001060	GATCGGGTAATTTAGTAATAGTTCATGAT ATTCATTACTCGGCGTAAATCAGGAAAAA CATTCTAGATGAATGTGGTATTCTCAGT GCACAGTTTGTTAGTTTAGAAAACAAAT	p001328	D	--
<u>443</u>	IM001061	GATCGAGGAGGGGAAGTCCTTCCTTCCT TCCTTCCTTCCTTC	p001329	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>444</u>	IM001062	GATCGGGGGTTCAAGGTCCTCCTCGGG GTACCTATTAGGAGGGCAGCCCAGGCTA CGTGAGACTCTGTCTCAATAAAAAATAAA ATAAAAAGCTGGGTGGTGGTGGCGCAC GC	p001330	R	--
<u>445</u>	IM001063	GATCGACCTGCCTCTGTCTTAAGCAAGA AGGGAGATAGATATGCATAGTATTTAGT GTAATGAAAGTTACGTTGTATTACGCTGA GGTTTATCACA	p001331	D	--
<u>446</u>	IM001064	ATCTAAGTAGTATAATGTTTAAGACGATC	p001332	D	--
<u>447</u>	IM001065	GATCGTCGTCTAACTTAGCTGGCTTTATA GTGATATAACAAAATATTAGAGGATGCTT TGGTTGAAAAAGAAGTTTATTTGCATCAC AGTTC	p001333	D	--
<u>448</u>	IM001066	GATCGAACACGCTCGGACTTGCTAAACG TTTCC	p001334	K	<i>Nmyc</i>
<u>449</u>	IM001067	GATCGTCATCATTTTTATAACAGTAGTGA GGAGATGTCCCCTGGGGCCGCCCTGGC TCTGGAGAGGGAAGCCACATGCTCCAAG GGGCTATGGTGAGGACCACAGCCTTTAC ATTTGGCTT	p001338	D	--
<u>450</u>	IM001068	GATCATGCACTGTCTGGGATAGTGATGG GCTGTGTCCTTTGTTGGCCAAGAGGAAG TGGCAAAGGCCAAAGTTGCTGTTGGCTC CAGGAGTCAGTCTGGGGACGGGGCTGA GATGCTGTGGGACAGACTCTGGAAAGG GCAG	p001339	D	--
<u>451</u>	IM001069	GATCGTGGCCACTGAGAGACCTTCTTCT GGCCACCAGATGCACACAGCTGCATGAA CATCTGCATACACATTTAACACATACAAA GTTGAAGAGAAGCACGTGTGTCTTGTGG TCTGACCACTTCTGGGCACCACCAAGC TGCTCTGACAACGGATTCCCACTGGGTT CGGCCATCTTGCTTCTCCCTCAGAGT TTGCCCATGTCTCTGTCTTTTCATAGCC ACAGCCTTGCCCAAGATAAGATACATCC AACTGTACAGTGCTCCAT	p001341	D	--
<u>452</u>	IM001070	GATCGTACCAGGAGCTCCAAGCGTACCC CTGATGCTACAACCTCATTCTGAGCCTT GATTCTGTGGACTCTAG	p001342	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>453</u>	IM001071	GAACAAGGAAGGAAATAAAGAATAAAGG ACATCTGACACTACCAAAGTTAGGTCAG GATGTGTCTTACAGATGGCCACTCAACA GCCTATAGAAAGCACCGCACAGACCAGC ACGGTCTTTTTCTCCCAGGTGTCTCTGA GGTACTGCTTCTTTCCAGGGATC	p001344	D	--
<u>454</u>	IM001072	GATCCCGAGTCCTTTCATCCTGTGGTTC TATTGTCCCCTAGGGCTTCAGCAGGCAG AAGGAGAAAGACACTGTAGAGCAGCCCC CAAA	p001345	D	--
<u>455</u>	IM001073	GATCCTGGGATTTTCTGGGCAATTGGAG GCCACAATTTAGATAGTTTCCGGAATCG ATGTCCCTTAAAGACCAGCGCCTGGACT CTACTGAGTAAACTCCCATTTCAACTTCC TCCTCTTCCTCTATTTGAACAACGTGTAT CATTAAATTATAAAATTGTTGTTGTTGTTG TTGTTGTTTCAAAAATTAACTTTATTGGG GGAGGGGCAGTTGCCCGAGGACAACCTT GTGAGAACCAGTTTTGCCTTCCACACT TAGGGGTCCTGGAATGGAACCTTATGT	p001346	R	--
<u>456</u>	IM001074	AGAGGAGAAATGGGGGTGCGAGAGGAC AAAGTCTGTGCCCCACAGCGCTGGGGC CAGAGCCCAGGAGGGCCTCATGGGAGA GGTTGCCTGAAGGCAGTAAGAGAGGCCA GAGGATGCTTGGGCCAGAGAGGTTCCC CACAATTGCTTGGATC	p001348	D	--
<u>457</u>	IM001075	GATCCCAAACAACTGGAACAGGGTTAT CCCAAAAGCTGTTGCCTG	p001349	D	--
<u>458</u>	IM001076	GATCCAACCTCCTCTTCACAAAGAGACTAT GTGCAGGATGGAGAAGAAGATGTATCCA AGCATATCCTGTGAAATTTATGTCAATGC TGTGAAATTTGTCCAGCACTCACAATCC AGATTTCTGCTTTTTAGGTGGCTTTTTCT ATTTCAATTTCTTCTGGCTTCATAGAAGTT TGAGGTGACATTTTAAAGACCTGTGCCA CTAAAATTTACAGACCCTATTTG	p001350	B	Mm.1238 02
<u>459</u>	IM001077	GATCGGTTAGTTTGACCAGCCATACTATA ACTTTAGTGCAACCCTTTACTTGGTGGGT GGTACTAGGAATTAACCCAGGACCTTC ACATATACTACTATCATTGAGTTACATTT CTAGCCCTTTTAACCAATTTCCCTTTAAC CCTTTTTATCCTTTG	p001351	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
<u>460</u>	IM001078	CTCAAGATTCTGTTGTCTGAGAATCTCTC CCTCTGCTTGGGGACCCATTTATAATGA GGTGATACTTCATCTGAAGTAATGGCCA GGCCACGGTGTGAGACTCTTGAATGTCA CATGCTGGATC	p001352	D	--

TABLE 2

SAGRES #	SEQUENCE	SEQ ID #	CLASS.	GENE
IM000127	CATGTGAGACTTGTTAATTTAGATTT ATTCTGTAGTGTTTTGATATGAGTAT AAATAAGACAATTAAATTCTATATTAG AAAGTGGCTTTTTACATTGAATATGC TTTCAGGATATGCGTGAGAATTTGGC GATGTGTAATC	4 <u>461</u>	D	--
IM000128	CCTTACTGCAGAGATGACTCGGCCA ACGGCTNCGAGCTCCTGACCACTTC CTCAGGTTTGGTTTTGTTAGTTTTTC TCACAGCAATGGGAAGCATAATCAAT ACAACTTCCCAGAATGCGACCTGTG ACAAGACCAATGAGCAGACTCAAGG CTGGGCACATAAAAGCACCAAAAAA AAAAAAAAATTCCCTTGCAATTATTGT TCATG	2 <u>462</u>	D	--
IM000129	GCTGCTCATCACCAAAGGAAGTCAG GACTGGAAGTCAAGCAGGTCAGGAA GCAGGAGTTGATGCAGAGGCCATG	3 <u>463</u>	R	--
IM000130	CATGGCAAGATGGAGACTTTGTCTA CCAGGGCCACTCCAAGCACCCAGCT G	4 <u>464</u>	K	<i>Fgf3/Fgf4</i>
IM000131	GTGAAAGGGCAGAAATAATTCCTGA AGGTTGTCCTCTGCCTTCTACATG	5 <u>465</u>	C	--
IM000132	CATGACTATGTTTCTTTTAGGTATATC TGAATAGTATGGATCTAAATGATGAA GTTACACCATTTTCTACAAATGGGCA CAGAACACAGGGCATAGATACAAAT GGCAAGGTGAACCCAGATCTCTGTG CTTATCTGCAATATAACAACACTAAG AAATATTAGGTCTCTCTGTGGTTTTT CTTAAATCTA	6 <u>466</u>	D	--
IM000133	GTATTTCTGTCAGAGGAAAAGAGTT TTCAAAAACTTTTAAAATTTTATTT GTTAGCCTGGACCAGTTTCATAGCAA CCTGTCATCCATATCCTCAGATTAC TTATGAGTTTGTCTGCCCATTAAAGAT CTTTAAATGGTTCTAACAGCTTACT TCATTGTTCAATTAGTAAAGGGTTTAT ATCTACACTTTGATATTTGCTTACTCC ATACATG	7 <u>467</u>	D	--
IM000134	CATGAGATGAAAAAGAACCTTTTGGA	8 <u>468</u>	D	--

	CTTGAATTTTGTGCTTCAAATGCGT ACTGCAGTTGATGGAAATT			
IM000135	AGGGTCCCTTCAACTTCCTCAGAGC CAAGGCTGACTTACTACCGTTCCCC AAGATCTCATG	9 <u>469</u>	D	--
IM000136	CATGCCTCTGGAAAGTACCTTAAACA TAGAATCCCCTCCCTAGTG	40 <u>470</u>	K	<i>Myb</i>
IM000137	CCAGATCCCATTAAACAGATGGTTGTG AGTCACCATG	44 <u>471</u>	K	<i>Wnt1</i>
IM000138	CATGACTTCTTTCATTTCTTCTGTGT GTCTGTCTTCCTGTGTTTGCCTGCCC CTCTCTTCTCTTCTAACAGCCCCCT TGAACCAACTGATGCGCTGTCTTCG GAAATACCAATCCCGGACTCCCAGC CCCCTCCTCCATTCTGTCCCCAGT	42 <u>472</u>	K	<i>Braf</i>
IM000139	CATGGGAATGTAATGTATTAATGAAT ATTATATAAAAGAGGCTAAATAGCTT GGCTTTAATTTCTCACTTTGCCTACT CAATTGAGAAGTTTATGGATCACCAA AAGT	43 <u>473</u>	D	--
IM000140	CATGTCCTTATTCTAGGAAGCCCCCT TTTTTACCCCTGCCTCTGAGAGAAAC AG	44 <u>474</u>	D	--
IM000141	CATGAACACCCAAATCCATATGAATA CACACATAAAATATTTTATTTTCTCTA TAATTTATGCCACC	45 <u>475</u>	D	--
IM000142	GAAAGCATTGAAATATACTGGCCTTA TTAATGGCACATG	46 <u>476</u>	D	--
IM000143	CATGTGCACACACCCCAAAATGAC CTCAGATGTCAGTGGTACTGAAACT GAGAACTGATGATAGAGCCAGTAA AAATACTGAAAGTGCCTGTTTTGAGA GTTTATATTTTACAATACTTTAATATC TAACTACACACACATACACCTGAAAA GGGCTCAGAATACACAGGCCTGAGA TGGCTCTCAAGAACCAGCCTC	47 <u>477</u>	D	--
IM000144	GGCCTTCCACTGCTCAAAGCTCAGA CTGCAGAAAAGGTTGATAGCCTCCC AGGGGCAATGACACCCTTTCTGCTT GAGCTTCCCCCCCCCCCCCTCTCAGG ATGTAGTCATG	48 <u>478</u>	K	<i>Wnt1</i>
IM000145	CATGCCAGTCCACATCTGCTTCTATG ACAAATGCCACATCCCAACGACAAA CTCACTCATTCTTCTGTATCAATTTA CGCATACACATAATACTTTTGCTCAA GGTACATTCATATTTCCGGCAAACAG	49 <u>479</u>	D	--

	ACAGCTATAG			
IM000146	CATGTCACTCACTTGGAGAAAGAGTT CTAATTATTTATCACGGCATTITTCAC AACTATAGAAATAAAGTTAATTTCTTT GGAAATAAAGTTGAAGTTGTAATTTT CAGATGGGCTCAGGTTGCTGTT	20 <u>480</u>	B	Mm.605 52
IM000147	CTCCTCCTAAAAGAAAAAGGAAAAG AAAAGTTAAACCTGCAACAGCATCAG CAGAGCTCACCCCTCCTCACCTGCA GCCCTGGTTGCCTCTCTTCTTTTCAT G	24 <u>481</u>	D	--
IM000148	GAAACACTGTTCTGGGTTTCAGGGG TTACTTAGCCTTGAATCAGAGTCTA CCCAGAGTCTACCTGCTTCTACCCAA AGCAGGTGGAAGAAGCTGCCCAGGA CGGGGCTCAGAGTCTACATTTGAAC TCCCTGTGCCAAGAAGTCTGGATAG AGTATAGTGTCTGTATATTCTAACTT TCTGGAACAACCCCTGCTTACAATAC TCTTTCCAACCTCTCAGGCCATG	22 <u>482</u>	D	--
IM000149	ACCTCTGTGCCAGCTTCTCGGACATT TAACAACTCTGGATCATG	23 <u>483</u>	K	<i>Fgf3/Fg f4</i>
IM000150	CTGGCAGTAACACACTTAACTGCTA GCACCTGGGAAGTGGAATAAGATC AGGAGCTCAATCAAGGTCATCCTCA GCTAAACAAGACCCCCCCCCAAAAA AAAGAAGAAGATGGCCTAGAAAGAG AACTCAGCAGCTGCTGATCTTACAGA TGACTAGAGTTTGGTTACCAGCACC CACATG	24 <u>484</u>	D	--
IM000151	CATGCCTGGTCCCTGCTGAGTGCAG AAGAGGGTGTGAGATTCCTTGGAAC TGGAGTTATATACAGTCGTGTGTCAC TGTGGGTGCTGGGAACTGAACCTGT GTCCTCTGCAAAAACAAGAGGTCTT GGTTGTTGTTGTTTGTGTTGAAACAG GGTTCTCTATGTGGCCCTG	25 <u>485</u>	C	--
IM000152	GCAGGAGCCCTTGTGCAGGCCACAA CCTGCACAGCTGTACAAGGCCTGCC TGAAGCTGCAACAGATGTGTGGGA TCTTGCCCCCTTGTGCAGGCGTAC AGATGCAGACTGCTCAGAGACACAC ATG	26 <u>486</u>	K	<i>Fgf3/Fg f4</i>
IM000153	CATGGGCTAGACCTACACTGAGTTG TGCTAAAGAAGTGAC	27 <u>487</u>	D	--
IM000154	CATGTCCTCCACAGCTGAGCACCCCT CAACTGTCTCCAGGGCCTCTGTTT TATCCAGGGTCTGCAGGGTCTCTGC	28 <u>488</u>	K	<i>Fgf3/Fg f4</i>

	CCCACGCCTAGCCCCTGAGAAATCT TAAGCAGTCTGAAAACCTACGCCACT GAACTGCTAAAACCCTGGAGTCACT GATGGAA			
IM000155	TAGTGCTAGACTCTGCCTTTTACCT GGCATAGATTACCTTTTCCAGATA TCCAGGGCACTTGCAAAGAAGCCAG GCATCATCAGGGGTTTGGACTTCCA GCCAGAGTCTGAGTTGTCACTTGAAT GTGCTGCATTTTGTGGATTGAGCCC CAGTCTCCCGACTCTTTGTGAGTTTA GGATAATAATCACAAACAGCACCCCTT CTTATTTGATGGCTAATAAGCTCTAG GCCAGTGTCTTAGCTCCATTTCATG	29 489	D	--
IM000156	CATGTATTCTGAGAGTAGAATTTATA CCCAGAGAATACCTAAGAAGTGAAC TGACGCCGGGCGTGGTGCCGCACG CCTTTAATCCCAGCAGTTGGGAGGC AGAGGCAGGTGAATTTCTGAGTTTG AGGCCAGCCTGGTCTACAAAGTGAG TTCCAGGACAGCCAGG	30 490	D	--
IM000157	GCCTGGTGTGGTAGCTCACACCTTT AATCCCAGCACTCATCTCTGTGATTT GCTAGGCCAGCCTGGTATACACAGT GAGTTACACATCAGCCATG	34 491	K	<i>Fgf3/Fgf4</i>
IM000158	CGACATCCAACCTTCTGGAAGGAGAG ATGGGAAGGGGCATTTGGGGTGCTA GGAAGGGATGGGAGGTGTCCCTAGA GCAGTGCTCATG	32 492	K	<i>Wnt3</i>
IM000159	CATGAAATAATGCCTTCAGAACTGCA TTAGAAATCACAAATAGCCCTGAATG CCCTCTAGATGCTTTTCTTGAGAAC ATTATGTGTTAAAGTCCTAAGGCCCT TGTAGCCCCACCATATGGAAAGGGA GAACTAACTGAAATGGGAGTT	33 493	D	--
IM000160	ACTGACAAGAATAGAGAGAAGTTCA GTCATG	34 494	D	--
IM000161	GTGTCCTGCTCCTGTCTGGGTCAAG GTCATAAAAGATGAGCCAAGGCTGA CTTCAGTGCCCACTGGGGAGACTG ATGTCTTCACAGGAATGCTCACCTG GAAGGTGTCCTCTGGGTGCATCTGT GTCACATTCGGTATAGAAGGAAGAAT GCCAACAATACTCTAAAAATATTAGA GGCCTTGAGAGTCCTCAGTGGTATT CCACCAACATCAAAGCTGCATCGTAA TATGCCAGCCTGGTCCTCACCTTTCC TGCCCTTCCCAGGAAAACATCAGCC TTTAACCTCAGCCCATAGGGGACAT	35 495	D	--

	G			
IM000162	AGGATCTTATAAAAATAACAGTGACC CAAAACATAATTTTTGCCATCAAGAA TCTCAAAATCAAGTCTCATCCAAGTC TACTCTTCTTTATTGTATCTTAAACAC ACACACACGCACACATCACACAAGC ACACACACAAGAATTACACACATAC ATG	36 496	K	<i>Wnt1</i>
IM000163	CATGGTATTCTGATGATAGTACCAAC ATACTGCTGCAGCTAGCTGTATCTG GAAATCCCAACCTCAGCCAAGTATTT GTGGTTGAAATAACCTATACTTCTCA CATCAAACAC	37 497	D	--
IM000164	ACTGTGACCTGAGCACTTCTTGTCTT ATCAATAGCTCACGTGCCAGGCCG GGTGACCAGTCTCTAGGATGTTCTC CATG	38 498	K	<i>Fgf3/Fg f4</i>
IM000165	CATGCACACAAACTGGCCCTGAACT TTTGACTTCCAGGCCTCTGCCTCTCT GCGCGCACACACACACTCGCACTCC TGTATATGAAGCGTATATGTGTTTCT CTGGGAACTGTTTTTATCAGGTGAAG CACTTCCTTTGTTCTTGCTACCCACC TCCAGGGCTCCAGGATCTCCAGACA GCCAACCCCTAAGACAGGCCAGCTT CCTCTGTATCTCTGTGATGAGAACCT TGGCATAGAGCTGCCCTCACCCCTCG GGATAGGGCTTATGTTCCCCGGAAC GAGCCAGGCACCTCAACAGCTCCTG GGGAGGAATAGGGGACT	39 499	K	<i>Fgf3/Fg f4</i>
IM000166	CATGGCACTATGAAGGAAATGAAGA TACAAAAGATTTCCCATACAAAGGGT CAACTGTTCAATTTGGCATTATT	40 500	D	--
IM000167	CATGATAGAAGACCACGTCTGGGAT GGGGTAAGGGTTTCTCAGAGTACCT TGCCCTGGGGCCACATCCTAAATCT ACAACAAAGCT	41 501	D	--
IM000168	CATGCAAAAGAATTCCAAATGATTTT ACAGATCTTAGCCCTCTAAGAGATAG ATATAGCACAAAGTCCTGACTCCTGAG GTAGGTACACACTGACTTCCTTCCAC AAGCACTGCCTCAGCCCGGAGATGA AGGTCACATCAATAGAGACAAAGTCA GGTTAACCGTGAGCAACCTCAAGAC AAGGAGGAGCACAGCATAGGTCGGT GGAAGTGTTTGCATAAGCCTAAGGC CTGGGCCCCAGTCACCAGCATTGCAG AGGAAAAGGAAAAACAGATAGTAGG TGCCCTTGGTGTGT	42 502	C	--

IM000169	CATGCAGTTTACCAATCTTTTTCCAC TCTTTAAAAAGACAAAAAATATTAGAA TACTGGGCTGAGGAATGGCTCATCA GTTAAGAGCGCTGCTCTTTTGAAGG ACTCCCGTTCTGTTCCAAATGCCAC CTGGAGGCTATCCTGTAGCTAGAGG T	43 <u>503</u>	D	--
IM000170	AGGAAGTGCTGAATAGAGAGGTTTG GGGAGAGCCCAACAATCTGACCTAT TTATACCCTGCCAGGCCCTGCCCAT G	44 <u>504</u>	K	S100a4
IM000171	CATGGTGCTGGAGGATCATCCATCC TGACATTCTGGGA	45 <u>505</u>	R	--
IM000172	CTTTAACCCATTTATGGTGTGACCAG AAACCACAGATCTTACCTAGGCTTCA GACACATCACCCGAGGAAAGCTCCA TTAAATCCTCATTCATG	46 <u>506</u>	D	--
IM000173	CATGTATTCATAAGTGGATATTAGCA AGAAAGTACAGGCTAAT	47 <u>507</u>	D	--
IM000174	CCTCTGGAAGTCAAGTGCAGCTTTG CTTATTTGTTTAAGCCATCCACCATC CAGTTATTAGATCTGAATTCATCTTT AGGGTCAGCTTTGTTGTAGATTTAGG ATGTGGCCCCAGGGCAAGGTACTCT GAGAAACCCTTACCCCATCCCAGAC GTGGTCTTCTATCATG	48-508	D	--
IM000175	GTTTTCTTTCTTTTTTTTTTAAAAGAA ACAGTCTCAAGTAGCCCAGGCAGTC CCTAAACTTATTATATAGCCCAGGAC AGTCTTGAATTCCTGAACCTCCCTCC TCTACCTCGTAGTCCTGAGACCGATT GCATG	49 <u>509</u>	D	--
IM000176	AGAGACCCAGAAATACCAAGGTGAT TTCCAAGTGCCTGACCTGGGAGGCA AGCATG	50 <u>510</u>	D	--
IM000177	CATGTAAGATCTTCACTTTTCCAGTG TCTGTTTGTGCTGCCTTCAAAGTGT GACCTGATGTAAAAATGTTTGCATCA GCTCAGGTGTATAGAATTGGACTGAT TCCAGGAGAGTCAAATATACAGAATA TCTAGTGTCCAAGAT	51 <u>511</u>	D	--
IM000178	CATGCTAATGGAGTTTATTCTTAGGA CTGCCTCCTGCATCCATTGATTGACT TAAATATGTGCACACT	52 <u>512</u>	D	--
IM000179	ACTAGGTGACTGTCTCAGGGTCTCA CTGTGTAGTCCTGGCCTAGAACTCT CTATGGAGACCAGCCAGACCTCACA	53 <u>513</u>	R	--

	CTCAGATCCAGATGCCTCAGCCTCC TAAGTGCTGGGATTAAGGCCAGTC CCACCATACCCTGCCCTGTTTCTGA CATTTGAACCCCTCCTTTAGACAGTA GGGAAACTGAGGCCCTGAGATATGA CACTTTTAGGGGCATG			
IM000180	AAACTTCAGAAAGCGGGGGCTACCA AGGAGACTCAATTAAGATCTCTCCTC GATCTTGAAACCATCCCCAGCCCTTC GCAAAGCACATTTGACGGACAGGGT TCTCTTGTCTTGGGCAACACATCCCG GCTACGCTCTGCAGGGTGAAGCTGT TAAGAACGTTCCATG	54 <u>514</u>	D	--
IM000181	GATAAGCCTCTACAAAGCTGGAGAG GGCAGTCCAAAGAACTTGAAAAGA TTAAAAGACAGTGCCTAAGGACACAA ACGTTTTTCCATAAAGAGCCTATGAC ATATTTTACTGCTGCTAATGAACTG ACCTTGAAGGAACAAGTGTTTAGGG TTAGCCTAACTTTGGAATTGGTGAA GGCAATGTGTCAGCTAGACAAATTA GAGAAAGAACTCAACAGATGAGTCA ATGAATTGTTCTAACTAGCTTGACT TAGGATTTTACGACACAGGAACAAAAG CACATACTGTCCCTCTGGTTGGCAT G	55 <u>515</u>	D	--
IM000182	CATGGAAAATGATAAAAACCACTC TAGAACATATTAGAGGAGTGAGTTAC CCTGAAGAACACATTCGTTGGAAAC GGATATTGTGTAA	56 <u>516</u>	R	--
IM000183	CATGCCCCGGCTCTATTACTATTTCTT TCTTTCTTTTTTGTTCAGGATCCAGT TTCCTTGATAAATTTTCTTGAATGTT GTTGTTGTTTTTCTTTGCTGAGTTT TTCTTCAATACTGCTGCTTTTCTCTC CAGGTTCAGGATGAGA	57 <u>517</u>	D	--
IM000184	CATGCTGTCACTAAGCTGTGCTCTTC CAAGGAGATGAAGAGACTAGCTGGT ACCCTTGCTATGCCAGGCTTTCTTCT TGTTTATACACACCTAATG	58 <u>518</u>	D	--
IM000185	CATGATCTAATCTGAACTTGATCCC AACCCTTTATAACAAGTGAATGTGT AATCTAACTAGTATAAGCTCTTGAA TAATAGCTGAGTGAATTGCCTTTGAT ACACGTTTCCAAATTAGTAGCC	59 <u>519</u>	D	--
IM000186	GTCAACCACAGCAGTACTGTTACTTT CTGTGGGGGAGACGTCTCCCCTCCT CATG	60 <u>520</u>	D	--

IM000187	GGCAGTGAGCTTGCCCACTCTGCTACAGGAC CTCGGTGACCCACTATATACAGCCCTCTTCA CTACGGCTCACAATCGGAGTTTAAGACCCAG TGAAGTAAACCCAGCAGGACCCCTTTACAAAG CCAGGACATG	64 <u>521</u>	D	--
IM000188	CTTGTCCAAACCAGCTTAGTCAACAG CCTCCTATCTGGGCTCCATCTTACCC TCCTCATCTAGCTGATGAATGTACCT GCCTTCTGTTCCCTTCCTCCTGGTCT GAGCTGAGCCTTCTTGGGACTGAGA GCCTTCATCCACCACAGGCAGACTA TCTTTAGATCATCATAGCCCCAGGTC TTCATTGCAGTGCAAAAGTGCAGAC CTTACATTTCCATTTTTATGCTCCCTT TGTAACGGCTCCTTACCGGACTGCA GCATAAGTGGCTGAGTATCCAATCA CAATAGAACACTTAGTTGTTTGCTTG TCTAACTCTCTCAGTTACACCATTGA GTATGTTACACAGGGCTGCTTTGTAG CTGTCACTGAGGCCACAAGGCAAGG GGACTAAGGCAGGACTCAGATGAGC CTGTTTTTACTTCCCGTTGTCCCTTT CACTTTGGGTTGAGCATG	62 <u>522</u>	D	--
IM000189	ATATAGACTCAATCAAGGTATTATTC TGGAACAAACAAGTAGTAACAAAAT AGTGCAATTGCAAGTATGATAACACA AGGCAGCCTTTACCAGCTTTGTCTGG AAGGAAATTGTTCTTTGAAATCTGAA TTCCAGAGAAAAAGTCAAATGTAAAC TAGAAGTGTTTGCATG	63 <u>523</u>	D	--
IM000190	CATGTATGTGCGTGTGTGAGTGCAT CAACACAAGTGCATAGATGCGTGTG TGTTTGTGTGTCTGACTGTTTAAGTA GGTGGCATCTGTCCTAGTCCTGACT TTTGATAAGTCTACACGTTTGATAAG AGGATCTCTCTCACCCTCAGGTTCC TCCCCCACCTCCACCCAGTACAC AGCCATAACTATAAACTCCCCACGCA GATGAAGCCCCCTCTGATCCCATTTTA GGGACATAACACCCCCCTCCCAGAC TGAGCTAATGCCTTGGACCCTCCAA AACTGATCTGAACCCTCTCTGACCCT GCCCTCCTCCCAGCACAGGGCAA	64 <u>524</u>	B	BF1638 10
IM000191	CATGATTTTCAGTTTTCTTGCCATATT CCACGTCCTACAGTGGACATTTCTAA ATTTTCCACCTTTTTAGTTTTCTGTCG CCATATTTACGTCCTAAAGTG	65 <u>525</u>	R	--
IM000192	AAGTATGTCTGCTATGAGTCAAAAGT CTTATTTTTGCATCACATG	66 <u>526</u>	D	--

IM000193	CATGCCGCAGTGGCCAGCAGCCCTG GTTCCAGCATTCTCAGAGATAACAAG GAGCCAGTGACCCCTTTCTTCAAGCA CCAAAGAAAAGCTAACCGACCCAC AAAGACCTGAGTATGAATGGTTTCTG CAGCTAAGGCACTTCCTTTGAGGTC AGCGCAGTTCGGGGCTGAGAAAAGA GCTTGCCCTGGCTTAGAGCCTTTCT CTGGCTCACTGTCCCAGCCAGGACC CATCCATCAGCCCACAGTGGGGTGG CATAGTGCAATCCTAGAGAGATGTTT AAAGGGACATATC	67 <u>527</u>	K	<i>Fgf3/Fg f4</i>
IM000194	ATTCTCTGGGTTTTCTGTGGTGCTC TGGACCCCTCTCGCTCCTACAATCCT TCCTCCCCATCTTCCACTGCTCTGCC TAGTATTTGGCTGTGAGTCTCTGCAT CTGTTTCCATG	68 <u>528</u>	R	--
IM000195	CATGCCCCTCTCGACCCTGGGAGCA TTCACCATCTTTATAAACTGATTCTTT CTGGGAAGATGATG	69 <u>529</u>	D	--
IM000196	CATGAAACACACTTTTAACTTTCCAC ATACTTTTAAAAGTGACCTTCCCAT TTTTTCGCCCTAGACCCAAATTGGA TGTTTCTGGCTCCCTCTCGTTCGTAG CTTTCCTGTGATGTAGAAACCTCTTA GAAACCACACC	70 <u>530</u>	D	--
IM000197	GTTTCCCACGGTGGAAGAGGCAAAC AAGATCCCTTGGGCCTGCCTTCTTGT GGCACTAATCTTACTCATG	71 <u>531</u>	D	--
IM000198	ATGTGGTGTTTAAATGAGAATGTGGC CCATAGGCTCATATGTTGAATACNTA TTTTCCAGTACTTGGAAGTATTTGGG GAGGACTAGAGGTGTGACTTTTTGA AGGGGGTGTATTATGTGGATGTACT AAGAACCCTTTAAATCCCTCTGACCAT G	72 <u>532</u>	D	--
IM000199	GCATCATAGTTGTACCATG	73 <u>533</u>	D	--
IM000200	CATGGGTAAACAGTGGGCCCTAAAC TTGAACTAGAAAACCTTAAAGATG	74 <u>534</u>	K	<i>Wnt1</i>
IM000201	CAAGTCTGTCTGTCTCCTTACTAGCC TTTTGCTGTTCTGACTCTCAAATGGT TCCTTAATTGGCCATTTGTCCCCTAA ATTAGGGGCGATTAGGATCAACACT CAAGCAATGTTCCAGATGGGGTCTG ACGTTCTCACTGGGGTCCCAGGGC TCCTCTGACTTGGTCACAGAAAAGGT CAGCCCTCTGACCTGGCATAGATGT CTGGATGACCTCTGACCTCAGCTCA	75 <u>535</u>	K	<i>Fgf3/Fg f4</i>

	TAAACCTGACTGTGGAGATTGAGACT GGAGGGACTCAGGGCAGTGGCTCA CTGGACAGTGCCAGGGTGTGCAGTG GTAGGCAGACTTCTATGTCAGGTCC TCCTGTGCCTCCATG			
IM000202	GCACATATCTGAGCATCTCAAGAAG CTGAAGCAGCAGAATCATCCGCTCG AAGCAAGTGTAAAGCCAATAAGAAGA CTCTGTCTCAGAAGAACTGAAACGA AGAGAGACAAAAACAACCTTCTGGGG CTGAAGAGATGGCTCAGCAATTAATA GCCCATTCTGCTCACTCAGAGGCC TCTGTGAGCTGTCTCCAGATGTTTAA CAAGCACAGCTAACATTTGGCATG	76 <u>536</u>	R	--
IM000203	CACATTCATTAAAGAGACTTTATTA GCTCAAAGCACATATTGCACCTCACA CAATAATTGTGGGAGACTTCAACACA CCACTTTCATCAATGGACAGATCATG	77 <u>537</u>	R	--
IM000204	GGGAGAGGCTTCAATGAGCCCCCT CACATTTGCATTTAAATAGCAGCATC AAGCGCTTCGCGTGCCACACACCAG TGGGCTCCAGATGTCAAGCCGGAG TCAGTCAGATGGCCAGTGCCAGCT GTCCTCCCTATGTCGTGCCGGAGCA GGCAGTGACCTTAAAGAGACAGCGC TCACCGCTCCTGGAGCCCGACTCTG GGTCCCTCATG	78 <u>538</u>	D	--
IM000205	CTTGTCCGCCACCCCGCCTGCCTCA TTACCTGGCTCACTCACTAACGTGAA AGCCTTACAGAAATCTCCAGGTCCTC AGCGGGAAAGGAAGTCATCTTCTTC CTCATCCTCGGAGGACAGAAGTCGG ATGGTAAGCATCTGTGCTGTGCTCCT CTAACTGTGACGCCGGGTTCCCATC ACATG	79 <u>539</u>	K	<i>Braf</i>
IM000206	ATATAGTATGACTGCCTCAAAACAAA ACAACAACAACAAAACCCCAAGATAT CTAAAGGAGGAACATTCCAAAAGAC AGAAATGTCCATAGACCTTGACAAAG GAACATG	80 <u>540</u>	C	--
IM000207	GTCAAGTGGATGTTTCTCATTTTCAA TGATTTTCAGTTTTCTTGACATATTT ACGTCCTACAGTGGACATTTCTAAAT ATTCCACATTTTTCAGTTTTCTCGC CATATTTACGTCCTAAAGTGTGTAT TTCTCATTTTCCGTGATTTTCAGTTTT CTCGCCATATTCCAGGTCCTTTAGTG TGCATTTTCGATTTTTCACGTTTTTA GTGATTTTGTCAATTTTCAAGTTGTCA	84 <u>541</u>	R	--

	AGTGGATGTTTCTCATTTTCCATG			
IM000208	CATGAAGTTAGAATAATTGGGATAAA GCTTTTATCATTATCAATTGGTTTTGA AATTATTGTATTGATATCTTGTAACCT GAATATTTATTGGTACATAAGTCTGG TTATGGTTGACTACTTTAAGTTTTAAG AGTTTTGATTCTTCCAGGTAAATGGG TGTTGTAATG	82 <u>542</u>	R	--
IM000209	CATGCAGCCGGGGTGGGATTTGAAG ATTATGCCTAGTGAATATTTAATATTA AACACGGTGTGATCGAATTGATAGCT GTTGAAACTAGAGCGAAACC	83 <u>543</u>	D	--
IM000210	GGACAGGGTCTCTCTCTCTGTTGTT CATTGTTTCATATATCATCGTCGGCC TGCTTACAGACTGCATTGTGTTCCCC TGTCTCTGCCTCCCATCTCACTGTAG AAGTAATGGGATTACAGATAGATGCT ACTGTGTCTGAAAGTTAAATTCCTAG GCCCCATG	84 <u>544</u>	D	--
IM000211	AGTGGGAGGGAGCGCCACTCTTGGA GCTAGGCAGGAAGTGTGTTACTTCA AAAATAACAAGACAATCTCACATTC CTGAGCTGAAGACCAGATGCAGCCA GGGACAGGGTTCTGCCCTGGCCACT AGATGGGCTCTCTGGCCCTGCTAAA GCACTGCACAAAAGTGGACGAGGTG CACCAAGAGTCCCGTGTTTGGCCCT CAGGGCAGACTAGAGAGCAGGACTT TCTCCTGGGAGCAGAACTGAGCCT GGGTCTTCATG	85 <u>545</u>	K	<i>Fgf3/Fgf4</i>
IM000212	CATGCTCATAATTCTGCAGTGCCTTC TCATAACACAGGATAAAACACTCTAA CCTTTAACATTATACTTGAAAATTAT GTGGTTTTTCTACCAGAGTCATAT CAAACCAAGTCTCCCTCTCCACTCACA AGGATCCAGTCACAATGGCCTTTTA	86 <u>546</u>	D	--
IM000213	CTGTAGGACCTGGAATATGGTGAGA AACTGAAAATCACGGAAAATGAGAA ATACACACTTTAGGACGTGAAATATG GCGAGGAAAAGTGAAGAAAGTGGAA AATATAGAAATGTTCACTGTAGGACA TG	87 <u>547</u>	R	--
IM000214	CATGGCGAGATTCTGTGTCCAAGCT GCCTCTACTCGTGACATTCCAAGATG CCTCTGAGGTGGGAACTGTGAAATA GGACAGAGCCCCACAGTCCCCTCTT	88 <u>548</u>	K	<i>Wnt3</i>
IM000215	CATGGGGGGGGGTACCAAGAAGGG ACTGCTGTGATTGGGATGTAAATAAA	89 <u>549</u>	D	--

	TAAATAAATAGAATAAACAAAACCCA AAAACAAACAGAAACCTAAACTCAAT AACTGCAGAAATGACTCTTGCTCTTT TCTGGTAAGGTTAGAAGCAGGTTAC AAATCTATATTAGAGATGGAGGCATT TCACACCAGCATAGGTATAGGAAGT AGATGAAATGAGGACTACACTAGAG TCTGTTTGTCAACAACCAATTCTGAGT GATTTCACTGAGATAT			
IM000216	CTCTGAGAAACCTACCCCATTTCTCCC TCCTTTCTCCCATAGCAACCACCTC CACAGCATTATCAAAGACTGCTGAC AGATTGGTGGCTCAGCAGGGAGAGT CAGAGCTGTTTCTTAGGTCTAAGTTG TAGCTCCACAGTAGTATGTTCTCCAT G	90 550	D	--
IM000217	CATGGAACACTCAAAGCTGGCCAGG GCCCATTTACCAGGTATCCTTTGCCT TCTCAGCTGATGGGCATCAACACATT AATTCACATATGACTCGTTTGTGTCA TATCAATAGTAT	94 551	D	--
IM000218	GTGGTTTTTTGTGGTAGAGAGACACA GAAGAAACTGAAGTCCTTGGAACATA ATTATCACTGTGGTTGAATGTTTGTG TTCCTATAACATCCTATGTAGGAAC GAACCTATAAAAGTAGTGGCTCCGA AGGTGGTGTCTTAAATGTGAACTG GGCTACAAGATTTTGCCCTTGTGAAT GGCTTTATGGAAGAGGCTGTCACTTT TCTGTCTCTTCCTCCATTATCTTGGA AGACACAACAGTTCAAGGTCTCATCT GGGAAACAGAGACCTTTACCAGACC CTAAATCTGCCAGTGGTGTCTTGATC CTGGTCTTTCTGTCTTAGGAGCTAT AATGCATG	92 552	D	--
IM000219	GGCCACAGCCAGTCCACCTGTATGC AGCTGGGTGCTTGGAGTGCCCTGG TAGACAAAGTCTCCATCTTGCCATG	93 553	K	<i>Fgf3/Fg f4</i>
IM000220	CCTTAGGGCCCAAATCCTTCCTCC CATTCTTCCATAAGAGTCCCCAATCT CCATCCACTGTTACCTGTGGGTGT GTGTATCTGTCTAAGTCAGCTGCTAG GTGGAGATGCTCAAAGGACAACATG	94 554	R	--
IM000221	GACAGTAAAGAAGACAAAGAAGTGA GTAGAGCTGGATGAAAAGTAGGAAG TTCAGACAAAGACTGCGGGAATGAN GTGTAGAGTCTAGAGCCCAAACAGT TAAACATG	95 555	D	--
IM000222	CTGCTACATTCTTAGCTCTAGCTAAC	96 556	R	--

	TAGCATCAATTGTCCCAACCCCTTCT ATGTATGACTCCAAAGCCAGTGTAC ATG			
IM000223	CATGGTCTCTAGAGCTAAGAGATAC CAATGCTGCGGCAGGCAGTTTTTATT ACAATCATTACAGTTTTGACAGTGTC TGGCCGTGTGCCAAGGCTGGCCTTC ATCCCTGAGCTCGGTGATGCTTCTG TCCTGGTCTTCTGGCTCGTCACAGC TTAAGAAAGTAGCTGCTTCTC	97 <u>557</u>	D	--
IM000224	CATGGAAAATGATAAAAACCACTG TAGAACATATTAGATGAGTGAGTTAC ACTGAAAAACACATTCGTTGGAAACG GGATTTGTGTATATCAATGAGTAGTT A	98 <u>558</u>	R	--
IM000225	CATGGAAAGATAATGTGTAAATTTGG GTTTGCCGTGGAAACTTTGTTTTCT CCATCAATGGTAATTGAGAGTTTGGC TGGGTATAGTAGCCTGGGCTGGCAT TTTTGTTCTCTTAAGGTCTGTATGAA GTCTGTCCAGGATCTTCTGACTCTCA TAATGTCTGGTGTAAAGTCTGGTGT ATTCTGACAGGCCTGCCTTTATATGT TACTTGACCTTTTTCCCTTACTGCTTT TAATATTCTA	99 <u>559</u>	R	--
IM000226	GGTAAGAGTGGGAGAAAATGGGGGT GGGGGGTGGGGACACTGCAGAAAC CTGGGAGAAAAAAAATCCAATAAAA TCAGGAAACACATG	400 <u>560</u>	D	--
IM000227	CACCCCCATCCCGCAGTTCCCAGAG GGAACAGTCCCAGCAAAAATACATG	404 <u>561</u>	D	--
IM000228	CATGGAGATGCAATGAAAGCACACA ATATTGCTGAACCAAACAGAAAGCTC AAAAGTAGGCACAGAAAAGAGATAC AAACACAAATCTGAACAAATTGACCT TCTCCCTATAGCATAACTAATATCTC AGAGATAAAAGTGGTCTTTATATACC AGGGCGAAAGAGGTCTAAAAGAGA GGAATAAAAAATATGGCATATTTCTT GTCATATGCAGAACCTATATGAGTCT TTTTGTTTGTCTTTCAATACAGCCT ATGTAGCTCTAGCTGTCCTAGAACTT ACTTTGTAGACCAGGCT	402 <u>562</u>	R	--
IM000229	CTGTTCTACAATGCCGGTTTCCAACG TATGTGTTTTTCAGTGTAACCTCACTC ATCTAATATGTTCTACAGTGTGGTTT TTATCATTTTCCATG	403 <u>563</u>	R	--
IM000230	GACAGGCTCCAATCAGATATACCAA	404 <u>564</u>	R	--

	GGGCAGGAAGCACGTGACAAAATCA GATGCCTGGAGACAAGTGTAATAAA AGAAGCAACAGAAAAACAAGGTTACTT GGCATTGT CACAACCCCACTCTCCC ACCATAGCAAGTGATGGATACACCAT CACACCAGAAAAAGCAAGATATGGAT CTAAAGTCACTTCTCATG			
IM000231	CATGGGTCCCTGAAGGGTCTCTCCT TTAGCAAACCCCTGTACAGTTGAAGT GANTTTTCAGGTACCCATTGGTCTTA GC	405 <u>565</u>	D	--
IM000232	CCCCACTCCTCACAGGGCTCCCCAC ATCTGCCCTGGGACACCCCACTCCT CACAGGGCTCCCCACATCTGCCCTG GCACCCCTCCATTTTTCAGGCACCT GAAGTCCCTACTTTCTAAAGGCCATT CTTCTACCTCAGGTCTTGCTCTAGGA CTGTCAACATG	406 <u>566</u>	K	<i>Fgf3/Fg f4</i>
IM000233	CAGGACAGCCAGGGCTACACAGAGA AACCCTGTCTCAAAAAACAAACAAC AAAAAAAAGACCATTATGCATTCTG CGGCTCTGACATG	407 <u>567</u>	R	--
IM000234	CATGGGCAGCACCTCGTGGAACT ATTATAAGTGTCTCCAGTCAGGTCA ACAGCGTAAGAT	408 <u>568</u>	D	--
IM000235	CCTGTACATTCTGTGTTAAGGACAGA GGGCCTCCTGCATG	409 <u>569</u>	K	<i>Fgf3/Fg f4</i>
IM000236	CATGGAGGCGCAGGAGTTATTGTCT AAAGTTGTGAAGATGAAGCCTAGATT GTATTGGAGATCCGGGTAT	410 <u>570</u>	D	--
IM000237	GCAGATATTTCCACCTCTGCCTTCCA CAGTCCTTCTCCCATG	411 <u>571</u>	C	--
IM000238	CATACGCTTACAATGTGTTGTTATTT CTGGTTCTCGTCTGCCTTCTTTATAA AAACAAATCCACTAAGGTGGAGTAG CCAGCCTTTACTCAGGGACTGTCAC CATG	412 <u>572</u>	D	--
IM000239	TTCTGTATATATTGTGTGGTCAGAAA ACCGTGGTTTTCTGGTGTCAAGAG TTAACTTTTCAGTAATCACTCATTCT AAACCAGACAAACCTTTAATCTTTCA TCTGGAAAGGTACTCATTCAAACCAA TGCTCTCTTAAAACAGAGTATTTAA ACAGCCAACCTGCATCTTCAGGGTTTC ATAGAAAATCAGCTTGATCTAAAATA GTCACTGAATTCTGATATCATAGACA TG	413 <u>573</u>	D	--

IM000240	TCCACCCACCCACCCACCTGCCAC CCAGACAAATGTTCACTGAGCATTCA TATACTCCATTCACTTCTAAGTACAG AGCCTAAGAATATGAGAAAATCCTCA TAGCAAAGAAATGCCTCTTGCAACTC GAGTAAAAACTCGAGTATGGGATGG AAGAGTTGAGAAAACAGATGATAGTA TGAGAGCCTATG	414 <u>574</u>	D	--
IM000241	AGGAGCCTAGCAGAATTGCCCTCTG AGAAGCTCCACCCAGCAGAAACAAA TGCAGAGACCCATCGATAAACACTG GACAGAGCACAGAGTCTTGTGGAAG AGTTGGGGGAAGAATTGAGGAACCC AAATGGGATAGGGACTCCACAAGAA GAAAAAGAGAGTCAACTAACATG	445 <u>575</u>	R	--
IM000242	CATGTCCTACAGTGGATATTTCTAAA TTTTCTCCTTTTTTCAGTTTTCTCGC CATATTTGAAGTCCNAAAGTGTGTAT TTCTCATATTCTGTGATTTTCAGTTTT CTCGCCATATTCCAGGTCCTACAGT GTGC	446 <u>576</u>	R	--
IM000243	CATGTGGAGGCCAGAAGTCAACATA TAGTCTCCTTCCCAATTACTTGTAC TGGAGAGC	447 <u>557</u>	D	--
IM000244	GTTCAGTAGCCAGCAGGGGGGATAG GACCAGCCCAAATTCTCCCTTTGCTT GGCCTTGACTACTAGTCTGGGAAGG GATAAGTGGGCTAACCAGAAGTCTT CCACATCTCTAAGTGATTA AAAATGG AAGACGTGATCTCTGGTCATTCATAA ACAGGCATTTCTCAAAGTTGGTCTGT GCAGTTTGTGGGAAAAAATGAAATGT ACTCATG	448 <u>558</u>	D	--
IM000245	CTACAGAGTGAGGTCAAGCTCGAGG ATAGCCAGGCAGGGATGCACAGGGA AACCCTGTCTCAAAAATCAAAACCAA CCCAACAAACAAAAACAAAATGGAA GGATAGAAGAGAGATAATCCATG	449 <u>579</u>	D	--
IM000246	CATGTACTGAATCCCTGAAGTTGATG CTGAGCACCATCTTGTGCTGTTCTAC CGCATTTACTGGGG	420 <u>580</u>	D	--
IM000247	CATGTGTCACTCAAAGGCTGCTGAG AATCAGGCTGTACCTGTATTCCTAAG CCATCCACAGCCATCCTGACCCACA GCAATGCTGGCAGTCGCCCCACAG CTGGACTCCGTTCTCCTCCCTCCACTC CTATAGCCGAGGCTATCCACACAGG CTATTTCAGTGCCCTAAGCCTTGCTA CCCTTATGTATACATTGAGGACAATG	424 <u>581</u>	D	--

	AT			
IM000248	AGAAACCACTGCCAAATCAATACATT TTAATTGGAAGTGTTTATGAAGCCCA GGAGAGATCCCTAAATGTATTAATTG CTTCCTGAGGAAATATAAACTCACA GTTACTAAAGCCATG	422 582	C	--
IM000249	ATCTTCTACACAGATGAACTGACAA AGTACAAATAAAGATTATATACCAA ATGAAAAAAGTAAACAGCACACATT TATAGATGCATCTAGCATCCCCAAA GCTCAACACCATCCATACTTGAAGAC TGCAGTGGTCCCTCTAGACAGTATG CTCCAGGTCAGCCCTCAGCACTTGA GAATAAACAGCTTCATTTACTCAGCC TGTTGTCAGGATCCATG	423 583	K	<i>Fgf3/Fgf4</i>
IM000250	ACTGCCTCAAAACAAAACAACAACAA CAAAACCCCAAGATATCTAAAGGAG GAACATTCCAAAAGACAGAAATGTCC ATG	424 584	C	--
IM000251	CATGAGCTGTCGATAGTGACCTGCAGTCAAG GAAATCTGAGGGCTTCCTAATTAACAGAGGA GCTCTAAATGAGAGTAACGCGCTCCACAAAC CCCCCTCAGACTCGGTAAGTGTCACGGTGCAG ATAAT	425 585	C	--
IM000252	GCCGCGTATGTGTTTCTTTTCATAGAAGAAT TAGCACATAATGGAATGTGCGTATCTGAAGT GCACAACCTGAGGAGTATTTATTATTACATACC TTTACAAGATATCTTTCTCAGGGAGCAACCT GAAAACATAAGGAGAAAAACATAAGAACTGC CACTCTAAGGGTTGGTGAAATGGCACAGCCT GGCGGTAGGACACACACATG	426 586	D	--
IM000253	CATGGAGAAACCTGGGCTTATTCAAGCAGTT TCCTTTGTTTACCCTGCCAGGGTTGCCAGT GAAGGGGCTCCTCCATCACTAACTAAAGGTC TTATCCTATGCTGGTTCCTCTCCACCCACCA T	427 587	D	--
IM000254	TATAGGAATAGAAATTCAGAACTTATCAGTTT GTTTTGCTTCAAATGTCAACACATAATTTAAAT TTACAAACCCCTTGACATTTGCATG	428 588	C	--
IM000255	GAAGACAAAAGATGTGTCAAATACCTGGGCA AAAGGGGGTGGTGGTGCTCTTTTCCAACTC CTGAAAGACACCTCTGCTCAGCACACTAGTT TCCAGGTTCTGGGTTAGGATTTGGGTGAGA TTGGTCGGCGATGGTTTGGTTCCTCCATTCT GCTGCTTCTCCCTGATACATTGAGTTACAGCA GCCACGCGTACACACTCTCGCACATG	429 589	K	<i>Wnt1</i>
IM000256	GAAGAGGAAATAAGGCAATAGCTAGACTGGA AAAACGAGCCAGCCTAAGAAGCTGCAGAGTA	430 590	D	--

	GTCTGTGGGGTTCTGCTTTGGTTAGCTGCCT TTAGTGCTCATG			
IM000257	CATGGATAGAGGATGGAAGTTGAAA ACCTGCTATTAAGAACATAGCCCTGT CCATTAGTGAGAGTG	131 591	D	--
IM000258	CATGTGGCCCAGGGGCACTTGGAGCCTTAG ATAGCTGCCTTTATGGCTCCTGGTGGCCTTG GATGTGGGTGGGTGACAGGAAACAGGAAGA GCTGGATAGTGGGGGGTCCCCAGGAGGAGC TAGCTGTGCTCTCTATCACTTTTGTCTCTCTG GGGCTACCCCCGTCTCAGGGGAAGGCCTGT GACTGGCTAAGCAACAAGTGTGGGCTGAGAC CTTTCTCTGTGACACTCTGGTGCTACTCTGG CCATAGCACAGATCTCTAGGAACGCACTCT	132 592	K	<i>Fgf3/Fg f4</i>
IM000259	TATATGGATATGTTTATGTGAGGGTAGGCACT CCTGGAGGGTGGAGGCATTAATTAGATCCTC TGCAGGTGAGCCACCTGACATG	133 593	D	--
IM000260	ATATGTGGACTGTAGTCATCTTGAACATCTGT AACAAAATATATAGATTAGGAGGTTTAGACAG CAGACATG	134 594	D	--
IM000261	GTGCCTCTTGCTGCGCAAGCTGGTATTGTAG CATG	135 595	D	--
IM000262	ATTTGTGACATCTTAGGAGCTTAGGTTGGTCT TCGAGACACAGGGCTGTCCCCTGTAAAGCAG GTTCCATCAGTGACTCCAGGGTTTTAGCAGT TCAGTGGCGTAGTTTTCAGACTGCTTAAGATT TCTCAGGGGCTAGGCGTGGGGCAGAGACCC TGCAGACCCTGGCTAGAACAGAGGCCCTGG GAGACAGTTGAGGGTGCTCAGCTGTGGAGG ACATG	136 596	K	<i>Fgf3/Fg f4</i>
IM000263	CATGACGACTTGAAAAATGACGAAATCACTAA AAAACAA	137 597	R	
IM000264	CCTAAGTCTGACCGTGCCACTTCCCAGTCTT CCCTACACTTCAATGCTTTTAGGCACAACAAA TTTGTACCCCTCATG	138 598	B	Mm.102 899
IM000265	CCCCCAGCCTGCTCCCTCCCCGGAGGGAG TCCCCAGTGACATG	139 599	D	--
IM000266	GTTTAGGTGATAGGGTACTTGCCAGCAGTA GGTGGTGCCAGGATTCTATCCTCAAATTG CACAAACAGAACATG	140 600	D	--
IM000267	CATGTTGTGTAGATACCTACATAATTATAATT CATAACTGTAATTTGCTAC	141 601	D	--
IM000268	CATGGGTTTGAGCCTTGTCTGAGCTGGAGG AAGAGAGTGACCCAAAGGGACCTTGGTAGCA GCCAGGGATGTGTTGGGGAGCAGAGAAACT TTTATGAACTTCAGTTTCAGTACTGAAACTTC	142 602	D	--

	CCTTTCCCTAGACTTCCTTTG			
IM000269	CATGGGACAACTCCTTTTCTTCTGGGTCA GGGGAGAGAGACCTCCTATCTAACTGTATA GGCCATTGCTGTAGCCCTTAGCTCACTTCCG GGGCGGGGAGGAGGAGGTTAAGACCCTAT	143 603	D	--
IM000270	CATGAAATGAAAGAACAGAGTAGCAATTTGG GGAGAAAAGCCTGCCGAGCGGACTTAATCTT TCCCAAGTGCTATCAGT	144 604	D	--
IM000271	ATGCTTGTCTTTCCCGCCATTACCTGCTTTT GTTTGAGATAATAGTTTTGTTACTTTATCAACT AGTAGCGACTAGTTTACATTTGGTTTCATAAA TAAGATCCATTTTAATCTGAGTTTTCCATCCTT GATTTATTTTGATTCATATTTAATTGTCTAGT TCCCATCCCTGGGCAGGACTTTTTGGGAAAG TCTTGCAGGTGACTATGTTGAGAATGATTTAT GTTGTATTAGCACAGGTACATTCGACAGTGC TGGTTCCTTCTGGAGCGCCTCGGGTGTGGGT CCTTTTCCTCAGC	145 605	D	--
IM000272	CATGAGTTTGATTATTTCTGAATTCTACCTC TCTTGGGTCTATTTCTTCTTTTGTCTAGAG	146 606	R	--
IM000273	GGGATAAGACTGGATAGTAAGCCGGGCGTG GTGGTGCGATG	147 607	D	--
IM000274	CAGAAGGTAGTGTTTCACAACAGTCCTCCCG ATGATCAATTGTTTACACTAAACCATATAGG AATTCACCCTGAGAGGAGTTCGAAAGCCTTT CAAAACCTGTACTGATATAAAGCAAATCTCTT TTGGATTCCCAATCAAAATGATTTGGCAGAAC TTTAAGGCCACAAAAATTGTGTCTGAACAACC CCTCTGAGCCCAGTTTTGTTAGCTTAAATTA GGGCCATG	148 608	D	--
IM000275	CCTCAAATAAGAAGCATCCATTTCTGAAGCT GCTGGGATTAAGGGAGTATGCCACCACCACC AGCTATGGCATTTTTTTCTTTAATTTTACTATT TTTTTGCTTGATATTATGGTTTCCAGTTTTGT GGGTTTTATAAGCTTTGAGTGTGTTTCTGCAT G	149 609	D	--
IM000276	GTCCACTTTAGGACGTGGAATATGGTAAGAA AACTGAAAATCATG	150 610	R	--
IM000277	CATGGTCAGCTCTCACTGCCCCATCCCCTGT CTCCAGTTCACGCACTGTATCCTGTGTCTTTC TCTGTGGCTAGACTCTTCTTGGGGGAGGG GAGTCTTGATATCGATGTGTGCTCACGCAC ATAGAGGCTAAAGATTAATCTAGGTGTATTCA TTCATCGTCTCATTGC	151 611	D	--
IM000278	CATGTGTTTCCTGATTTTAGTTGGATTTTTTT CTCCAGGTTTCTGCAGTGTCCCCACCCCCC AC	152 612	D	--

IM000279	ATGGTGTCTGTTTCATAGCAGTAAAACCTTAAC TAAGACACTGATATAACTCACCTTTCCCAGCC TCAAAGTCTCTACCATCTCAGGATCCACTCAC TCATTCACCAAACCTTCATCAAATGCCCACTGT GCTATCATCAGTACAGAATAAATCATG	453 613	R	--
IM000280	CATGAGACTGTCACAAGCTCCTGGGATGGGG ACCTTACCAGAAAGCCACCAAATCAGAGGCA TCCCTGTTTGGTGAGGGTACATTTGTTTTCC CCAGGCCCTGAGTGCCAGGCAGGAGCAGGC AAAGTTCACCTGGGAGGATGCCCTGGAT	454 614	K	<i>Fgf3/Fgf4</i>
IM000281	GTTTTGGTTCTTTTCAAAGAAAAACAAAGGTC ATTGCAGCTTTTTGTACCATTGAGGTGATGGT AGGAATTGAGATATATAATCTACTTGAAGATA TATATTATGGCATG	455 615	D	--
IM000282	CCGCTGCTCTCTCACCACCCAGTGTGTCTG CTTTTAGCCCAGACGGGGGAGGGGGTAAGG GGGTGGTCTGTCTCATG	456 616	K	<i>Wnt1</i>
IM000283	GTGTCCCTCCTGTCGTTAGGCAGTACTTCCA AATCAAACCATG	457 617	C	--
IM000284	AGCTGGTACAATGCTTAGAGCAGAGCTGCAG AAGCAATACAAGAGATCCTGGCTCAGCTAGG TGCAAGCTGGAATAGACTCCTGACAGTTGTC CTATGAACTCCATACACAGGCATG	458 618	D	--
IM000285	ATGGATCCCTGGGGGGCAGTCTCTGGATGG TCCTTCCTTCTGTCTCAGCACCAAACATTGTC TCTGTAACCTCTCCATG	459 619	R	--
IM000286	CATGATGCACTTAGCAATTCCTCAATTGAGAC TCAAGTGAGCCTAGGCTGTGACAAAATGACT GTAAAACT	460 620	K	<i>Fgf3/Fgf4</i>
IM000287	CATGTAAAGCTAGTTCAAAACATACTAAATAA TTCAGTTGTAGAAGAGGTGAGGTTATCTCACT GCCAGGATAAGCTATTGAACAAGCAAGGGTT CTCACTTACTGTTTAAGTGGAAGTGTTCCTT ACTTCAAAAAGTCATTAATGAATTTTAAGCTG CATAAATATTTAGTTATT	461 621	C	--
IM000288	TAAGCTTTTCTCTTACACAATCCCCCGGAAAC CCACAGTTTAGGTCACAAAGACCCAGGCACC TATTCCTAGGCCTGGTAAGTGGGCACCCACC ATTTACAAAGAGCTCAGCATTTGGCTCACACA TG	462 622	D	--
IM000289	CATGAAGATGAACCGGGCTTGTTTCTCTGGC AACTAGGCTCAGAAAGGATAGGACCACCAGC CGAGTAGCTGTCAGATGGAGCTGAAGACCTG AGGGAAAGAATGCTTGTTGGGAAGAAGCTGG CTCCTTTTGGTTTTGTTGTTGCTGGTTTTGTG ACCGGATCTTGCTGTGTGACCCTACCTAACA T	463 623	K	<i>Wnt1</i>

IM000290	CATGGACTTAATTTTACTGCATTTGAATTATG GAAAATATATATGAAAAGTCTTTAGAAAAAGG CAGAGGACGAAAAAACCAGAACTTTAATT ATCTGAGACCAAGAAAACCTCTTTAAGAAAAAG CAGTAGATTTAACTACGTGTTGTTAAAAATAG TCCTGTATAGATATAAAGTCCCTCAGAGGGA AGAGATTTGTTGAATAAATTCAGACACTCAAG AGAA	464 624	D	--
IM000291	ATTAACAGCCCAGTGCCTCAGAAGTGAAT GTTGAGAAGTGGGTAATCTGGGACAAACAG AGGGAAGAATAGTGCCCTTGGCACGTGCAAA GGAGTTTGGGAACAAACATG	465 625	K	<i>Fgf3/Fgf4</i>
IM000292	CATGTATGACAGTGAGGTCAGGAGTGCCAG GGAGCTTGCAATTGGCAGAACAGCCTTTCCTG GCCAAGCCTAGTGTCATCAAGTATATATTGGA CCAGACCTTATAAACTTGGGTTCCACTCTG GCTGGACCAGCCTCAAGGCGTCGCCTCTCC AGGCCTACCTCCCAGACGCAGAGGCAGCATT TGGAGGATTGAA	466 626	D	--
IM000293	CATGGGAACTTGTTCCAAGCAAGGGACTCTG CTACACCTTCAAGGGACGCTGCTAATACTGG GTTCAACCTTGGGCAGCGTGACAGCAGGA GTGGGAGGGCTCTGATGAGGAGAGCCACCC ACACTGTGAGATCTAGGAGATAAGGTCACAT CCAC	467 627	D	--
IM000294	CCCTCCAGCAAATTGAAATACGAAAGACTCA AACACATTAGAACCATTCCAATAAAAACTTGC ATTGCCCCAGGCCCTCCCACCACCATG	468 628	D	--
IM000295	CAAGAGTATATATCCAAGAAAAATACAGCTGA GTTGACTGTTAGTTCTGTTTTGGCCTTCATG	469 629	D	--
IM000296	GGTAAAACTCTACCAGTTAACTAC ATTCCCAGCCTGCCTCCAATGAATTT AATTTGTGTTTTTAGGGTTTCTGTTAT TGTTGTTTTTGAGACAGGGATTACACA AAGATCTGCCTGCCTCTGCTTCCTGA GTGCTAAAATTAAAGGTATGCATG	470 630	R	--
IM000297	GTTTAGTAAGTGTCTTCTGTATTACTTTTGTG AAAATTAGATTGTTCTGTGACTTTGTGTGC TATATTCTCTGCATG	471 631	D	--
IM000298	CATGTTTCTGCTTCTACTTTATCCACCCTGCA CACACTGACTGCTATGTTCTGTACCTTTTCC ATCTCTCCATTGAATATTCACCTCCAACAGTGG CATTGGAAATTGCAGTGGAGATACC	472 632	D	--
IM000299	ACGATGGTCTTGCCCTTTCTCACACCATCAAT AGTCACTCAGAGCTGTGGTTGTTATCTGAAG TGTGTTGCAGTCCAACCTTGCCCCATG	473 633	D	--
IM000300	GGAGTGTAAGCGTCGGTGTGTACCCGTGA	474 634	K	<i>Wnt1</i>

	GATTAAGTCAAAGTGACATG			
IM000301	TAGACCCAGTCTTGCACCTGGCCTGG GACTCGCTTATTAGGTTTGACTGTTA TCTGGCCAACAAACACCAGGAAATG GGGTGACAGGTGGTTGTGAGCCCTC TGAAATGGGCATTGGGACCTGAACC TGGGTCCTCTGTAAGAGACATG	475 635	D	--
IM000302	TCACCCAGCTGGGGCTGTGCTGAAGACTCT GAAGGGGAAGATAGGCCTATGGTNACATG	476 636	K	<i>Fgf3/Fg f4</i>
IM000303	GTTGGGCTGAGCCACAAGTACACCTCCACTC ACTGAGCCATCTAGCAGGTCCCAAACAAGGT GACTTTTGTATCCAGCAAGACATAGCCATCT ATGCCAGTCATCCTTGTGTCATG	477 637	K	<i>Fgf3/Fg f4</i>
IM000304	TAACATATTTGCTTGTTATGAAGGAAAATGTT GGATGTGTGTGCCTGTGGTTGAGTACTGCAA GTAGTGTGAGGGAAGAGAAACCTAGCTTGAA CAGTCCCTCATCTCCTTCATATCCTCACTCC TTGTCAGGCCCTGTATTAGGTAGTGCTTCCC TACCTCCCTAATGCTGTGACCCTTTCTTTAAT AGAGTTCCTCATG	478 638	C	--
IM000305	CATGTGAGCACAGGTACCTATGGAA ACCAAAAGTGTAGGATCCCTTAGAAC TGGAATTATAGGCAGCTGTACGCTAT TGATGTGGGTGCTGGAAACTGAACT CCAGGCTTCTTGAAGAGCATCAACT GCTCTTAGCTGG	479 639	D	--
IM000306	CATGTAGAGACTGCCATATCCAGGGATCCAC CCCATATCAGCATCCAAACGCTGACACCAT TGCATACACTAGCAAGATTTTATTGAAAGGAC CCAGATGTAGCTGTCTCTTGTGAGACTATGC CGGGGCCTAGCAAACACAGAAGTGGATGCT CACAGTCAGCAAATGGATGGATCATAGGGCT CCCAATGGAGGAGCTAGAGAAAGTAGCCAAG GAGCTAAAGGGATCTGCAACCCTATAGGTGA AACAA	480 640	R	--
IM000307	CATGTCCTAGAGTTGTTCCAGCACAGAAGCT TTTGGGAGAGACCACCATTAAGTAAACGCAG CAGATGCTGCAGCT	481 641	D	--
IM000308	CTGCTTGTTGTGGGGACCAGCCAGACACCTT CCACAGGTGCAGTGGTGCAACATG	482 642	K	<i>Fgf3/Fg f4</i>
IM000309	CATGATGTTTGTGAGGAATAGAAACCCTGA CTAAGACAGAGGATATTCAAGATCCAACTA GCAGGTTAGCTGTGGTTCC	483 643	R	--
IM000310	CATGAAGCACACATTACCCTGTGACTTGCTTT TTTATTAAT	484 644	D	--
IM000311	CATGTGTCCTCTTGCTTGAGTCTCTATTCT TTGTGATTCCGCAGCTCTCCATAGAGTGCAG	485 645	D	--

	TTCTATGTCCTGCCTGCAAGGTCCATTGGCTT ACTAGGGTCTGCCCCTCCCAGAAGAGTAGCT CATTTAGAATGCATTACTGGTGTGCTGTCTTG CATCTTTTTTACCCAT			
IM000312	ATCTATGTTTATGCACTACTAATTACTGTTTAG TTTATATATGCCCTAATAATTACCCCATGAAA ACTTAAATTTTGTTCAAAAGTGTGGTCTCATT GGAGGTGTTAATGTACAATGTCTTTCTCATG	186 <u>646</u>	D	--
IM000313	CATGGCCAGCTGAGCGGGCTGGAACCTGCC CTTCTGCTTCCTGTCCCTGCACCTCAGCACC GCTGTGCACTTGGTACTAGACCTCAATCACC GCAG	187 <u>647</u>	D	--
IM000314	CATGTGCGTCCCCCCCCAAACACGCAAGCGCA CACCCACAAAGAGAAGAGACAGGG	188 <u>648</u>	D	--
IM000315	CATGGCCACTTGGAGAGAAGGGGGAAGGGA ATGCGGAGAGAGCGGGAGCAAGAG	189 <u>649</u>	C	--
IM000316	CTTAAGCACTGATCAATGGCCAAGGTTTGCC GACTTGGGATCTGGGGTATAGACATCCACCC ACTGAGACCTCTAACAAAACCAGATGTGGA GGTACGAAGCCTGGCTCAGGGGCCTGTCCT TTGTCATCAGAATTCACCAGCTGCAGCTCCT GGGTCAGCTTTGTTTGGCATG	190 <u>650</u>	K	<i>Fgf3/Fg f4</i>
IM000317	GTGTATTGATATGCAAATGTGTTAAAATATGA TTTAAAATTCCCCATG	191 <u>651</u>	D	--
IM000318	GCAAAGTGTCCACACTTTGGTCTTCGTTCTTC TTGAGTTTCATG	192 <u>652</u>	R	--
IM000319	ATAGCAGGTCCTGGATACCCCAACATACCAG AAAAGCAAGATTCAGATCTAAATCACTTCTC ATG	193 <u>653</u>	C	--
IM000320	CATGTCCTGGCTTTGTAAAGGGTCCTGCTGG GTTTACTTCACTGGGTCTTAACTCCGATTGT GAGCCGTAGTGAAGAGGGCTGTATATAGTGG GTCACCGAGGTCCTGTAGCAGAGTGGGCAA GCTCACTGCCTGCTACCAGCAGTTCATATG TTTTATGGTCTGCTGCCTGCTGGTGGTTTATA GATGCTGTGTCGTAAGAGAAAAGTTCAGGGT AGCCTGGAGTGAATGGAGTTGGGGTATCAG GGAGGTCTTTGTACACTGGGGTGAGCTAGGC CTCTGGAAAGCTTCTGGGGGTTCCCC	194 <u>654</u>	D	--
IM000321	CATGCTCCAGGCACCAGGCTTGCTTTGCAT AGGTGGGACAGGGTCCCAATACTCAGCCTG GGGTGCCAATGAGGCTCAGGCCACACACCC TCTTGGTAGGAGTCACTGTAGTGGGGTCTGT GAGAGCCAGTAACTTGTGAGGGTGTGAACTT AGCTCAGGACAGAGGCCAGCAGGAAGCTTT CCCTACAGAGAGTGTTTTCGTCTTTTCCTTTT TCTGGTTTGTTTCTTGGGAAGGGAACAATTTT	195 <u>655</u>	D	--

	CGCTTTTAGTTGGCTTGTATTATTCGCTACTG AAACCTTAAG			
IM000322	CATGTATTAAGTCCCTCGTGAGGAA GGGT	196 656	D	--
IM000323	CATGAGTCAGAGGCTTCTACTCCAGTTAAAA CTGATCTGGGTATAGAATTGTGTTCTCAAGAA ATAGTAAGTTATAATCAACTAAGTCATCTCCT GTCTCATTTTTTCTTCCAAATCGGGTCCTCG AATTGTTATAAGAAGATTCAATCAATCAACAG TATCCCTTTCCCAATTTGTGTGCTAAGTGGA ACAGGTCTTAGCACATCAATCACATAAAGTTC AATTAAGAAGGAATTTAAAGATCAG	197 657	D	--
IM000324	GCTATGAGTCTCCACTTGTAACAAT TATACTCAAACATATTCAGGACACAC TTGGGCTTCCTCCATCAAGCCAGGC AGGTTTGTTTTCTTGTTTGTTTGAGA TAGATGGATGGGCCAGCTTCATG	198 658	C	--
IM000325	CCCACCCCTAGCAACCAGTTCCTCCTCTGAA TGGAAGACATCTGATACCACTTTGAGCTTTC ACATG	199 659	D	--
IM000326	ATCNNCGAATCATTCTAGGCTTGTGG GACCATG	200 660	D	--
IM000327	ACTATTCTCAACAATAAATGAACCTTCTGGGG AATCACCAATCCTGATTTCAAACGGTACTGTA GAGCAATCATG	201 661	R	--
IM000328	CCTAGGCACCCACCACAATAGTTAATCCATCT TTGAATTTTGACCCAGTGTTGCCAAGTATTC ATTGCAACAGCTTTTCAAATGTTTTATTCTTTC CCAAATAAATTCCATG	202 662	D	--
IM000329	AGAGGCTACCCCTCAAGTGGCTTGCCTAGT ATAGCTATTACAGACAGAGAACTTCCAGTAAT TTCCTCAAGCCACATG	203 663	D	--
IM000330	ACTCTGAACCTTGCTTGCCTGGTATTTTTGC CTCTCTTATCCATTGACCCTGTACAGAAAAG CTGAGGAAGCAGGTGCAACCAGGCATCTCA GGCACCCAGTTAAGAAGTAGATGAAATACTG TAATGTACATG	204 664	D	--
IM000331	CATGATTTTCAGTTTTCTTGCCATATTCACG TCCTACAGTGGACATTTCTAAATTTTCCACCT TTTTAGTTTTCTCGCCATATTTACGTCCT AAAGTGTGT	205 665	R	--
IM000332	CATGAGACAGTCCCAGATCCCTCACCATAAA GAGCTACCATATAC	206 666	D	--
IM000333	CATGCGACCATCCATCAGGAGTTGGAGGTGC CATCGGCTCTGCCCTACAGAAAAGGAATCTG AGATTTAGAAACCCAGGTGACCCACTCAGG	207 667	K	<i>Fgf3/Fgf4</i>

	GCCACCGGGGCAGTAAAAAGAATCTAAGATC TAAAGTCAGTGGAACTCCTCCCAACCAGCA GAGACTCCTCCCAGCCAGCTCTTGAT			
IM000334	GGGAAGCAAGAGGCAGTAAGAAAGGGGAAA CTGGGGAGGTAACCAAAGTCACATG	208 668	D	--
IM000335	CATGCTAACAAAGAATGGGGAAAGCTCTCTA GGCTTCCACCTTAAACAATGAGGAAGGGAAG AAGGAAAG	209 669	D	--
IM000336	CATGTTGGTGGGACTTTATGGGTATTGCTTCT GATATTACTAGGAGGCACAATCTCACAGAAA ACTCCCTGATCTTACAATCCTTCTGCCCCCTC TTTTGCAATGTTCCCTGAGCCTCAAGTATGGA GTTATTTTATAGCTGTATTCAATGAGACCAGA ATCCACAGGTATGC	210 670	R	--
IM000337	CTCACACAGATATGCATG	211 671	D	--
IM000338	AGAAGTGATCTTTCTTCTGTGTGCCCTGTCA CCCTGGGAGGCAATCAGACGGTCCCTCATG	212 672	D	--
IM000339	CTTTCCTTTTGTTTTGGACGAATATTATTGAAA TATGTAGTGTGCATG	213 673	D	--
IM000340	CATGAGATATGATTTTAGATCTGAATCTTGCT TTTCAGGTGTCTTGGCATATTCAGAACTCGCT GTGGTGGGTGAACTGGGTTCTGATGATGCCC ATTGGTGCTGGTTTC	214 674	B	AI5970 62
IM000341	CATGGAAAGGTATTTGGAAATAGGCTGTTTTG TGTGTAATC	215 675	D	--
IM000342	CCCTAGGACTCACCTGGTAGGAAAGAAGTAA TTCTTCCAAGTTGTCCCCTGACATCCACAAGC ACATAGTGTCAAGGCATG	216 676	D	--
IM000343	CATGCCATTCATACATACTGGCAATGGATATA TAGAAAATGAGACTCCTTCTAATATTGTGTGA TGACAGAT	217 677	D	--
IM000344	AGAAACCATTTACACTGCCAGGTTTGGGGCC TGCCTATGCATG	218 678	D	--
IM000345	GATCCCTTTAACTTCTTGATAGTTTCTCTAG CTCCTCCATTGGGGGCCCTGTGATCCATCCA ATAGCTGACTGTGAGCATCCAATTATGTGTTT GCTAGGCCCTGGCATAGTCTCATAAGAGACA GCTATATCAGGGTCCTTTCAGCAAACCTCTTGC TAGTGAATGCAATGGTGTGCATCTTTGGAGG CTGATTATGGGATGGATCCCTGGATATGGCA GTCTCTAGATGGTCCATCCTTTTGTCTCAGCT CCAACTTTGTCTCTGTAACCTCCTTCATG	219 679	R	--
IM000346	AGGGTGGTCTCTGCAACCCAGGCTGGAACC CAGCACAATAAATAGTTTTATTACATAACCG AACGCGTGGCTCTGCGGCCACATTCGGTGC	220 680	K	Wnt1

	AAATTATTTACACAGTGATGAGGAGGCAGGA CAGGAAGGGGTGGGAGGAGGCTGAGGGAG GCATG			
IM000347	CATGTGTGTTCTTTTGTGATTGGGTACCTCA CTCAGGATGATATTTTCT	221 681	R	--
IM000348	CATGAGGCCAAGGGAGAGGGCAAATTCCTGTG TGAATCAATTATCATCTCACAGAGAACATACC	222 682	D	--
IM000349	AGTAGTATGCCACAGGGAGAAAGGGTATTTA TCAAAGGGACAGGAGCTAGTTGTGGTGACCT TACCTATCTGCTTGCCTCTGCCTCCACGGTG CTGGGATTGAAGGTGTGCACCACCACACCCA GCTTCAGATTTTTGTTTTATTTATTGNGTATT CCTGTTTCACCTGCATG	223 683	R	--
IM000350	CATGCATATACAGGATATAACCTTTGTAAGTA AGAATAAAGCACATAAAAAATACTTTTCAGTAA TATTGTCCAAACCACTT	224 684	D	--
IM000351	CATGTGTGTGTTTGTGTTTGCGGAGTGTGGG GGCGGCAGGGAAAGGTGGCCAGGCTGTCAC TCAGAGATCAGGATGACAGGCGCTCCCTCAT CTAGGCGCGGGAGCTCTGATTGCAGATTCTGA GGAAACAAAATAGCAATTG	225 685	K	
IM000352	CATGAAGATGAACCGGGCTTGTTTCTCTGGC AACTAGGCTCAGAAAGGATAGGTCCACCAGC CGAGTAGCTGTCAGATGGAGCTGAAGACCTG AGGGAAAGAATGCTTGTGGGAAGA	226 686	K	<i>Wnt1</i>
IM000353	TCAGTTCCAAGAGATGACACAGCCG CAGTCATG	227 687	R	--
IM000354	CAGAGACTGAAGGAAAGACCATCCAGTGACT GGCCCAACTTGGGATCCATCCCATTTGAAAG CATCAAATCCAGACACTATTACTGATACCATG	228 688	R	--
IM000355	CCCTACAGTGACACTTACTCCAATAAGGCCA CACATCCTAGTAGTGCCAGTCCCCATG	229 689	R	--
IM000356	GGCCTCTATTCTCGGTTTCAGATTAAGTACCTG GCTTCACTGAGAGCGGCTCTTTTCATTCTCTAA ATGGTTCTCATG	230 690	D	--
IM000357	AGTAGATGGCAGAGAATAATCAAACCTCAGGG CTGAAATTAACCATG	231 691	R	--
IM000358	CCAACCCAACAGCTGGGAAGGGTTGGAAGTA GCCCCGAGGCTGGTTAGTCCCCTTCAGATG GGGAGGTTAGACTGGGGCTAGCCAGGCTGC TCCACATAGACTTCCGATTTCGATTAGAAATG AAAAGAGGAGAGGAAAGGGAAAAGGAAGAA AGGCTACAAGCATG	232 692	C	--
IM000359	CATGGGGTCTGGAGCCAGCTATCAAACCCAG GATTGTCTTAAGTGTGGTGGCTTGGATGAGA	233 693	R	--

	ATGGCCGCCATAGGCGCATAGATTGAATTC TTGGTCCCTAGTT			
IM000360	ACGGTGGGCTGATATTTCTAGATCTCCTAGT GCCTATCCCCTATTATCATG	234 694	C	--
IM000361	CATGAATTTTGAGATATTCTCTGAAC CAAACAATATT	235 695	D	--
IM000362	GGAGAAATTATGCCTTAAATTA AAAAGCAAAT ATTGAAAAATTAAATATAATTTCCATTAAATCA TAATGGACCAACAACAGAACACATCTATCTAT GTATCTATCTATGTATCTATGATTTATCTACC TATCTATCTGAAAAGCAAAACTACATG	236 696	D	--
IM000363	GCAAGGACAACCTGACAGTTTGAAGCAACTAT TTTCATCTTGACTCTCACTCGGCTTTTAACGT CCATTGAGGAAACAGGCATG	237 697	D	--
IM000364	CATGAGAAGTCACAATTCCACCACTT AAAATCAGTGCTTGAAGGATACTGT AGGCCAAGAGGTAAGTAGAGGGGAC AGCAGTGCACGTTTTTCAAAGTGTG GGTGTGTGTTTGTGGGTGTGTGTCT GTCTGCCTGTGCGTGTATGTGGGTC AGTACAGGAAAAGC	238 698	D	--
IM000365	CAAGATAAACTCTTAATGGGATTCTAGGGAGT CATTCTGTAGAGAGCACTTGACTAGAAGGTT AAGTCTTAGATCCAGATCCCAGCACAAACATA ATACATCCTATACTCACACACACACACACA CACACACACGCAGTCCTCATG	239 699	D	--
IM000366	CATGTCTCAAAAAAAAAAAGAATCACTTGGA TTGTACATAGTAGTTAATAATATGTAATTAGTC TAACTGTGAAGGGGCACTTATTAGTTTCTACT ATGTAGTGTAATGAACTATGTTGCTATTAGA AATTC	240 700	D	--
IM000367	GAAGGTTGAAATCTGTAATCTATCTTCTATGG CATCATTACCTCTCTAATACAGCTGTAGAGA AAAATGTCTGAAGATTGCGTTCTACTCTCGTT CTTTGAGGTCTCCCAACCCATG	241 701	D	--
IM000368	CATGGCTGGACTATAGAGCTCTAGCTTCAGT TGCTGGGATGTTCACTGCATCACCACAGAGA GGGTTCTTAAGTGGTGATGGTGGTAGTGGAA AGGTGGACCCTCCAGACAAAGGAAGCACTCA CCACGACCCTGCTCACCTGTGAACCTTTCTCT TTCAGACTGATTCTGAGATCAGCCAGGCAG GGCTACCAACCAGGGACTCGTAATGAAAATT TAGGCATATGG	242 702	D	--
IM000369	CATGGTCTGGTGAGTATGGCACCAGATAGGA TGTTATGCCC GTTTCTTATCTCAAGAAACAAG GAATCTTGTTTCTTATCATTAAATAGGAAGAAT AGAGCAGTCCTGGCTAAATGAAAGGTGGNAA	243 703	D	--

	AGTTGGTTTGAGTATCTCTTTCC			
IM000370	AAAATCCAATACACATTCATG	244 <u>704</u>	D	--
IM000371	CCCTTTGTTGTGCATTTAGCTAATCTCATCC CTGTTTGGGTCTGGAACCCTCTTGCTTCCC TGGCATCTAGGACTTGCTAGTGGCTACCCCC AGCTCCCCATTCCCCATTGCTACACACCTCT GTTCAAATTCCTGACCCTCTGTATATCATCCC AGTCTCTTCTAATACCTGACCTGAACCCCTT TTTCCCCTCCCTCTATTCTCTTCTTGCAAGT CCCTCCACCTTCTACCTTCCATG	245 <u>705</u>	R	--
IM000372	CATGGGTCATTTCTGATCTTTACCAAGCAACA GTGATGAATCTATAAATAGAACCATCAGTTCA AGAAACACAACCTTAGATTCTTTCCATACCT TGCTTTTGTTCCTTACATCTTCCCCCTGCCCT GTGGTTTTCTTTAATCTGTTTTTACAATCC AAATTGTATCCCCTTCTCTGTC	246 <u>706</u>	D	--
IM000373	TTGGGCCTTTCATACCCTGTTCTGGCTAAG ACAATTGTCACCTGACTGGGCATG	247 <u>707</u>	D	--
IM000374	AAGTGGATGTTTCTCATTTTCCATG	248 <u>708</u>	R	--
IM000375	TATAAGCAATCCCAAAATTCTACCTGGGAAC TCCTAGAGCTGATAACACCTTCAGTGAGCCA AGTATCTGGGTATAGGATTAATTTAAAAAAA TAGAAAATCAGTATCTCTTACATACAAATA ACAAAAGGGCTGAAAAGAAATTAAGGAAAT AAAACCCCTTCACAATAGCCATAAATAATATAA ACTATCTTGGGATAACTCTAACCAGGCAAGC AAAAGACCTGTATGATCAAATCTTTGAAGAAG AAAATTGAAAAGGTATCAGAGGAGGTAAAG ATCTCCCATG	249 <u>709</u>	R	--
IM000376	CATGGGCTCTGCTTAAGAAACCCCGGAG	250 <u>710</u>	C	--
IM000377	CATGCTTTTAGGCCTTTTCACGATCTTANNGG GGACCGNGAGAGNTNGCTGCTGGATGATCT CTGAGAGAGCTTATCGTCCTCAAACCTGCTGA TATTCAAGCTGTTTCGCAGCTGCAGCAGCAA AGTCCCGGTCTTTGTCACCGATCTGTGAACA GCAACAATGAGCACCTTTCATAACAGACAGG AAATGGATGCT	251 <u>711</u>	A	<i>mDal1</i>
IM000378	GGCGTACCTGTGTATATGCATGCAT G	252 <u>712</u>	D	--
IM000379	GTGCTAGGCTCACTCAAGATAAAATT TGCTATTTTCAGCTCCCTGGATAATAA AATCTATCCTCTCACAGCTGTGACTC TCACAGGGGTGCAGGCAGGACGAC ATCAAGAGAGTGATGGCCTCTAACA AGTGTCTGCCCCACTTCTCTTCCGG GTCAAAGACTAGATCTAGACTGGTG GGGCTGTTGATTCACTATGAATGTGC	253 <u>713</u>	D	--

	CTGACACCATCCCACACTTAGCATCA TAGACACTTGGGGGACTGGTGATAC ACTATGATGCCTGACACCATCCCACA CTTAACATCATG			
IM000380	CTATCCCGAGGGTGAGGGCAGTTCT ATGCCAAGGTTCTCATCACAGAGATA CAGAGGAAGCTGGGCCTGTCTTAGG GTTGGCTGTCTGGAGATCCTGGAGC CCTGGAGGTGGGTAGCAAGAACAAA GGAAGTACTTCACCTGATAAAAAACAG TTCCCAGAGAAACACATATACGCTTC ATATACAGGAGTGCGAGTGTGTGTG TGCGCGCAGAGAGGCAGAGGCCTG GAAGTCAAAAGTTCAGGGCCAGTTT GTGTGCATG	254 714	K	<i>Fgf3/Fg f4</i>
IM000381	GGGGTTGACTAGAAGAAGGAGGCGATTAGG GTGTATCATATGAGAGAAGAATAAATAAGGA AAAAATAAATTTACAAGGATTAATAAAGTAATTA CATACATACATACATACATACATCCATACATA CATACATACAAGTTAAACTGTTATGGTAGCAT G	255 715	D	--
IM000382	AGGATGATATTTTCTAGTTCCATCCATTGCGC TAAGAATTTCTTGAATTCATTGCTTTTAATAGC TGAGTAGTACTCCATTTTGAAGTATACCATA TTGTCTGTATCCATTCCTCTGTTGAAGGACAT CTGGGTTCTTTCCAGCTTCTGGCTATTATAAA TGAAGTTGCTATGAACATAGTGAAGCATG	256 716	R	--
IM000383	CATGCCTGCAGGTCACAGCCTTGCGCGCCTC CAGTGCCCGAGCGTTCAAAGTGACACAGACTC TGTCAGGATGGTTCAAATGCAAATCTCTGCAA CTGCGTTAGCCGCTTCTAACCAAGACAGAAA GCTGCCGTCTGTCTTCGTGTCTGTCCCCA TACCCCATATCGGGTAGCTTTTCTTTCAGCAT TGTCCAGACACCATCATATGCCTACATCGCA CAAGTTCTCTGAGGCCAGATAATTGGCAGCA CTCCTGTTGTGTGCCGAGAGTGCAGAAAAGG GCTATCCCGAAAAGGTGTGATCTGGAAGAA GGAAAAAAC	257 717	D	--
IM000384	ATCTTTTGGCCAGAGCAAGCAGGGACTGAGT GAGCAGAGGTGACAGGAGCGAGCAAGGCTG ACAAAGTCTTCCATATTCCTACTAGGATGACC CATTAAAGCCCCATTTAAAGCATTCCATTGCTT TCCAAATACAAAGTCCCAAATCCACATTCTT TCAAATAAAAGCATG	258 718	C	--
IM000385	TTAACATATGGTTTTTAAAAATCCATAATGAG CATATGATAGAGAAGTCATCAGAGCTCTTCA GCTCCACATCATCTGTCCCCAGAAGTATTACT ACTCCTAACTTGCTGAGCCAAGGCACAGATA TTCTTTGTGTAAGCATCTCTTCTTATCCTGT GTTGCCACGCAGGAGCACGCACACTGCTTCC	259 719	D	--

	TGTCTGAGGTTGTTCCATATCAGCATG			
IM000386	CATGCCAGGGCTTGAATTAACACAAGTGCCC CAGAT	260 720	D	--
IM000387	CCTGTCTGTATATGCACATG	261 721	D	--
IM000388	CATGGAAAATGAGAAACATCCACTTGACGAC TTGAAGAATGACGAAATCACTGGAAATCGTG AAAAATGAGAAATGCACACTGTAGGACCTGG AATATGGCGAGAAAACTGAAAATCACGGAAA ATGAGAAATACACACTTTAGTACGTGAAATAT GGCGAGGAAAACTGAAAAAGGTGG	262 722	R	--
IM000389	CATGAAGGTAAATTATGACCATCAGGGTTCA GACCTCAGCTCGACCGGAGACCAGCCTGCA ANTCCCCACAGCCCTCCCTAAAGTGGGTAA AAGACAGAAAAGAATTAATATCTGA	263 723	R	--
IM000390	CATGCACTAGCAAGATTTTGCTGAAAGGACC CAGAT	264 724	R	--
IM000391	GACACATACACACACATG	265 725	D	--
IM000392	GTAAATGTATTAGGTTGAGAACTGGCACTGCT CACTTATGTTACAGTTGTTTGGGTAAAACTA GAACCAAACACAAAAGCAAAAGAGCCAAGCA GCAGAGCAGGGAGCAAGGGGCTTGGGGAAA ACACTCACCTCTGTTGTGTCTTCTTAGCTG TCAGGGCATTGAGTGGCAAGGAGTGGAAAG GAACTTTGGGCATTCCGAGTCAGGAAAAGTG TACCAAATAACACTATGGAGGTTAGCAAGT GTTCTAGAGGGCAGAATAAATACATG	266 726	D	--
IM000393	GTTTAGGTCATTGGTGGTACACTCTCCAAGG ACAGTATAAATTGATTTTTTCTGTATCCTTCT TTGTTCTTGGCCATAAGGCACTTGGAGTGCA TTAATATGTACTTATTATTACTATGTCTTTTCT TGTCTTTGGCTTAAAAGAAACAGGGTCAAGT GACCATG	267 727	C	--
IM000394	AGTTTTCTTTAAAAAATAAAGTAGGAATGAA ACTGGAACAAAAATGCAATAAATTTAAACCA TCACCGCTAAACATG	268 728	D	--
IM000395	CATGATTTTCAGTTTTCTTGCCATATTCCAC	269 729	R	--
IM000396	GAGAGGAGCCTGGGGAAATGAAGGT CCAGCAACAGGCCCAAAGTGGGATC CAGCTTAAGGGGAGGCCCAAGGC CTGACACTATTACTGAGGCTATGGA GCACTCATAAAAATGGACCCAGCAT G	270 730	R	--
IM000397	CATGGCAGCCTTGGAGTATCAGGCT GCTGTTCCCAATGTGGGATGCAGAG GGCACTGCCAGCCTGGTTATCACGC ACCACTGTCACACAGGGAAGCGCCC	271 731	D	--

	CCTTCCC			
IM000398	GGAGTTCTTCTCTTCAATAACAGAGTAAATTC TCCCTCAGCAGTTTCTCCCAGGAAACCCATAA CCTAGCCATG	272 732	D	--
IM000399	CCTTAGATGTTTGTCTAATCGACAAAATACTT TATATGTGAAAAGGAAAAGCATG	273 733	D	--
IM000400	AATAATCAGATTTCCAGAGCTCCCAG GAACTAAACCAACAACCAACGAATAC ACATG	274 734	R	--
IM000401	ATCCAGTAATCATTCTTATTGTTTCCACA CAGGAAAACCTGTAATAGATGGTTCATCAGC TTTATTTATAACTTTCTATCTTGAAAGCAACTG GAATGCCCTTCAGTAGGTAAGCAGATACACT AGGCTCACCTCAACTATAGGCACAATGAAAG GAATGAAATGTCAACTCACGAAAGGTAAGTA CACATG	275 735	D	--
IM000402	CCTCGCCATATTTACGTCCTAAAGTGTGTAT TACTCATTTTCCGTGATTTTCAGTTTTCTCGC CATATTCAGGTCCTTCAGTGTTCAATTTCTCA TTTTTCAAGTTTTTTAGTGATTCGTCGTTTT CAAGTCGTCAAGTGGATGTTTCTCATTTTCCA TG	276 736	R	--
IM000403	CATGCAAGAACAGGACAAATGTCTGTGAAGA AAATGAGTGAGCGTGAACAGGAGGTCAAGGA TCCGGTCCCAGGCAGCTCTCAGTCTGGGCAA GCATTTCTAAACTTTGCCTTCCTTCCTGTTGG GGGTGAAGGTCTG	277 737	K	<i>Fgf3/Fgf4</i>
IM000404	AATAGGAGTAGATGAGAATGAAGATTTTCAA TTTAAAGGACCAGCAAATAGCTTCAGCAAAT TATAGAAGAAAACCTTCCCATACCTAAAGAAAG ATGCCCATG	278 738	R	--
IM000405	CATGCAGCCCCATTAGTGATTGATCCTGTTT CATATAA	279 739	D	--
IM000406	CATGGGCTCTCTGCTGATAATGCTG AGGCTGTTTGTGCTGTAGTCTGCGC TTTTTGCCCCCTCTCAGAAAAACTGT ATGTCATAGGAGTTGCTGGCTATTG GGTACATAAGCAAAGCCACCCTATT GTGCCAGTGCCTTAGACAGTGAGAC AAGAAAGGCCCTGGTTAGAAATCTT ATCAGGACTGGGAATGTAACCTCAGTT GATAAGAGTGCTTGCTTAGCGTGCA CACAGCCCTGGGTTCAACCGCCTAG TACTACAGAACTGAGTGTGGCTTCA CACACCTGTAATCCCAGCACTTGGA GAGATAGATGCAGGAGGATTAGAAG TTCAAGGTTATCTTTAGTCACATAGT ATTGGTAGCCAGCCAGCCTGGAATA	280 740	R	--

	CTTGAGATACTTACAGGAAGGAAGG AAGGAAGGAAAGAAGGAGGGAGAG AGGACAGGAGGAAGGAGATAGATAT ACACAGAAAGAGACAGAGAAACAGA GATTCAGGAGACACAAAGACATACG GAGACACAGTGAGA			
IM000407	CATGTGGTTGCTGGGGATTGAACTCAGGACC TCTGGAAGAGCAGTCAATGCTCTTAACCGCT GAGCCATCTCTCCAGCTCCCTTTAGACTTCT TAGTAGCAGCATTAAATTCTTGCTTGGTTTCAG TTCTGACAACCACAGCAGTCAGGAGTTTGAG TAAGAGG	281 741	R	--
IM000408	CCTCATAATGTTTGTGTTGAGCATTTTT TTAAAACCTAACTTGTCTTTTGCTTAT CTATTGTGGTTTCTTAGTGTGTGTGT GTGTGTGTGTGTATGCGCGCGTGTG CTCTGGTCTTCGTGCACATG	282 742	D	--
IM000409	ATTTGTGACATCTTAGGAGCTTAGGTTGGTCT TCGAGACACAGGGCTGTCCCTGTAAAGCAGG TTCCATCAGTGACTCCAGGGTTTTAGCAGTTC AGTGCGTAGTTTTAGACTGCTTAAGATTTT TCAAGGGCTAGGCGTGGGGCAGAGACCCTG CAGACCCTGGCTAGAACAGANGCCCTGGGA GACAGTTGAGGGTGCTCAACTGTGGAGGACA TG	283 743	K	<i>Fgf3/Fgf4</i>
IM000410	CATGTATGCACAACCAAACTTATAAATATGA GAATTCACCTATAGTCCTAGTCCTTTAATACA GAATTTAGCATTCCGATATAAAACAACAGATT AAACCCCAACAGTTAGAATAGAGCAG	284 744	D	--
IM000411	AATAGGAGTAGATGAGAATGAAGATTTTCAAC TTAAAGGGCCAGCAAATATCTTCAACAAAATA ATAGAAGAAAACCTCCCCAACCTAAAGAAAGA GATGCCCATG	285 745	R	--
IM000412	CATGCACACCCTACTCCTGGGTGATCGTACC AGCTCCAGCCTCTGTTCTGCACGCTGTGCCT TCAACCTGGCAACCTCC	286 746	K	<i>Wnt1</i>
IM000413	CATGAAAACCTGTCTCAGAAAACAAAACAC GTTGAGAGCCAGCATAGAAGCCATAGGAGGT AATGTGTGTGTGTCTGTATATATGACAAGAGC AGACCTGTGCTGAACCAGTTAACTACTTTTG	287 747	D	--
IM000414	CATGCTACTAACCAGTTGAGGCAGTACCAGT TGTTGAAGATGCTGTCTTTTATCCAATGGATG GTTTTAGCTCCTTTGTCAAAGATCAGGTGATC ATAGGGTGTGAGTTTATTTCTGGGTCTTCAGT TATATTCCATTGATCTACTGGCCTGTAATTGT ACCAATAC	288 748	R	--
IM000415	GGTTAGGAATTCTGGACAGTTGGTACTTGGT TTGAATATAGTAGGTGACAAGCTGTGCCTTG	289 749	C	--

	AGTGGGGTGGCAAGCAGGGTTCTCTGCAGC AGGATGCAGTGTACATG			
IM000416	CATGAAAATGTTAAGTCCTGACAGACAGGGT GCCATCTGCCAAGAATTTGAGTAATCTAGAAA CAGAAAT	290 750	D	--
IM000417	CATGGGGTTTTGTGGATCTG	291 751	D	--
IM000418	CAGAACAAATAAGCTGGAAAGGATGAAGCAG CCACAACATAACTGCTGTTGGCTTCTTTGTGT ACATTTTAAACCTTCCTCTGAAAGAGTGACCA ATGCTTTTAACTGCTGAGTTATCTCACCCGAC TTACTTTCTCTCTCTCTCTCTCTTTTCCTTCTT CCTAAAATTAATTGTGTGTGTATGTGTGTGTG TGTGTATGATTAGAAACCTTTATGTGGTGG TAGAAGACCATCTGCAGGATTCATG	292 752	D	--
IM000419	CATGGTCCCACAAGCCTAGAAATGATT CGTGGAT	293 753	D	--
IM000420	GGGGTCCAGGAGAGAACTTGAGTC ATG	294 754	D	--
IM000421	GGAAAGAGATACTCAAGACCAACTTTACCAC CTTTCATTTAGCCAGGACTGCTCTATTCTTCC TATTACTGCTAAGAAACAAGATTCCTTGTTTC TTGAGATAAGAAACGGGCATAACATCCTATCT GGTGCCATACTCACCAGACCATG	295 755	D	--
IM000422	GTCCTTCCCAAAGAATAGTGTTAACTGAGCTC TTTGGGTGGCAATAAATGAATTGCTCTGGTG GGACAGGCAGTGACATATGGGGAGGGGGA GACACATG	296 756	D	--
IM000423	CATGTTCTTACTTCTTGTTG	297 757	D	--
IM000424	GGGTATATGAATTATATATATGTGTGTATAT ATGTATACAGGCATG	298 758	D	--
IM000425	CATGCGCCCTAAGACTCATCTCCACGAATGA CGTGACGACCTAATTGCATTCTTCTAACCCA CTGATTAGGCAAACCACCTCCAAAGGGCTC GCTGAGTTCCTCTTCGGGAAGAGGTGTGTTG AGTACGCTGGAATGGATATTCGAGGGCTGAG G	299 759	R	--
IM000426	CATCTCTCGAGCCCTTGCCAGCCTTTTTTCT TAAAATTGTATTTTTAAAATTTATTTTCTGTAC ACAGGTGTGTGAGTGTGAACATG	300 760	D	--
IM000427	CATGTGGACCTGGGGGCTAAGTCAGGGTGA AGCTTCCACAGCTAAGTGGCTGGAGGCTGCC CTAAAAGCTCAGGAGGCACCGCAAGCAAGC CTTGAAAAACCTTACCCACCAGCTTGACCTTA GACTTCTGGCCTTCAGGCTGTGACAATACAT TCCTGCTGTTTAAAGAACCATATGGTTGGTGA TGTTTTGTTTCTGGTTCTTTTGTGTTGGT	301 761	K	<i>Fgf3/Fgf4</i>

	GTTTTTGTTCGCGGGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTG GCTAGAGATAAGATCTGA			
IM000428	GTCTAAAGTTTTCAAATGATGGATAAGTTGTT AAACCTCCTTTAAGATCTCAAGCACAAAAAGA AAGACATCAAATACGAATAGTAGAAAGGAAA GGAGATTTGGAAGTGTAGAGGCCCAAGAGTCA TAAAGAGAAGAATTTAAACAACTGTACCCACA AATTCATTAGCATAGATCAAGTAGTCCATTTC TTCATG	302 762	C	--
IM000429	CATGTATGTTCTCGATGCCTTGGCCT G	303 763	D	--
IM000430	AAAGACATTAACCTTTGAGAACCAAGGGGTA GGACAGTATAGACTGAATTTGCCTCCCCTCT TCATAAGTTGCTACTGCTAACCTCATTTCAGA ACTTAAGCATATAACCTTCATG	304 764	D	--
IM000431	CATGGAGAACTAGCAAGAGCAGGATGGCGTT TCTCTAGAATGCCGTATAG	305 765	D	--
IM000432	CATGGTGACTTTCCATCTTTAGAACCATAATC ANGTTTAAT	306 766	D	--
IM000433	CATGCTTATATCCCTCAAAAATTTTACAGTTAA ACTGAAAATGCTTACTTACTTTTTTTTCTTACT TATATCTAGTATCGATAAGAACTGTCCCAAAG GACAC	307 767	D	--
IM000434	CTGGGTCTTAGTCCTCTGAGGTCCCTAGCAC ATCAGAGGTTTCATCAGTTCCAAGAGATGACA CAGCCGCAGTCATG	308 768	K	<i>Fgf3/Fg f4</i>
IM000435	CATGGAGAATGCACAGTCAAAACGCTTGCAT CCT	309 769	D	--
IM000436	CACCCCCTCCCGCCTTACATCAATC CTGGGTGCACAATGGGACTGTGGAT GACTGATGTCTGCGCAAACAACCTTG CGGGGAAGTCTAGCTGACAAACGCT CATG	310 770	K	<i>Fgf3/Fg f4</i>
IM000437	ATGTATCCAATGGCAAAGCACGGGGGAGGCT TCATCTTGAAGAGAAGAGTGCTCTTGGTAGG CTATCCTTTTTTTGAGACAAGTAGAAATAGGA GCATTTCAACAATCTGGACATATGTCCTCCCA CAAGAACTTGTTGAGAATGGGTCTGAATTAAC TGGAATAAAAGTGAACACATTCTCCTATACA CATG	311 771	D	--
IM000438	TCACTCCATTTTAGTTCAAATGCTAC AACTCCTTTGAGCACCCTGTGCTTT CAAGACCTTATTCTGTGAATACCATG	312 772	C	--
IM000439	CATGCTTAGCCCAGGGAATGACACTATTCTGA GGTGTGGCCTTATTGGAGCAGGTGTGGCCTT	313 773	R	--

	GTTGGAAGAAGTGTGTCACTCACTGTTGGGG TGGGATTTGAGAGCTTCCTCCTAGCTGCTTG AGGATGCCGGTCTT			
IM000440	CATGAGCTGGGTGAACGACAGCAAAGTTTG TTTCTCTTTTAAGGAAGACAATGGTGTGAAAT TGGTTGATCCTTTGGGGGAAATGTTGGCCCC TT	314 774	B	Mm.202 45
IM000441	CATGATCTCACTGTGAGGGCTGGCTACCTTG GAGCTCACTGTACTGAAATATTCTGGCCGATT GCCTCTTCGCTGGGTTTATGGGCACACACAG TACTTGTCTATGAGTCTTTGTTAGGCTGAGCC TAGTGGTGCAGGCCTGTCATCTCCCCTACTT TACTTTAGGCTCTGAGGCAGGAGGAT	315 775	D	--
IM000442	TCTGGTAACTTGGGGGTCTGATAAAA CAGTTGGGGGATTTCTTTTCTTTTCG CGTCTGAAGCCAATGTTATTACAGGT GTGTGCTTGTCTCTCCACACCCCTG CCCCTGTTGCCTAACACACGCGGCA CACACATG	316 776	D	--
IM000443	CATGACTCTTCCTCCAGAGTTAGAGGTGGAG CCAGGACAAACTCTAAAGAAAAGAAACCCCA ATCAAAAAGGGAAGCTGGTATCATCCAACCT TTAAATTACTCCACATCCCTCCAGAG	317 777	D	--
IM000444	CATGTCTGTCCCAAAAGGAAGTTCCTTCCTCT GTCCTCCACATCTGACCAGCACCATCATTCA ATCTGCAACCCAAACCAGACATTTACATCATC TATGCCTCCTTTCCTGCTTGTCTCCCCTCAAC CAGCACCCAGCAAGCTTTCAGGTATCCCCTT AGTGTGTGCAGGATCTCTCCAGTTCTCCAGA CCCCAATTCTGTTCTCACTCTACACTGCTAGC	318 778	D	--
IM000445	AAAGCTAACTTCTCATCACCTACCTAATAGCC TGAGAGCCCTGTGTAGAAAAATTAAGGAGTT TAGTTCCTTCATG	319 779	C	--
IM000446	CATGCAGACAAAAGTAAATAAGAAAACAAATTA AATGTAGGCTGGACGGATAGATGGT	320 780	D	--
IM000447	CTCAGCTCCTAGGCAACACTTGTAGACCCAC AGCCCCCTTCACACACACACACACACACAC ACACACACACACACACGGCTGGGGATCCAAC CCATCTCGTCCTTACACGTGCTCTACCATCAC ACCACACATTTCCAGCACTTTTATCTGAAGTG TTTCCTTTTATTTGTGCATG	321 781	K	Wnt1
IM000448	CATAACCACTATAACCAGCCTGCTTACTTGGC TTTGTTCGAGGGCTTTTGTTTAGAGCTCTT TCTTTTACCCTTCTCCGTGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTCTGTCTGTCTGTCTGTCTTAGTGTGTGTAC ATG	322 782	C	--

IM000449	CATGTGGTCCACGGTTTTACTTTACTAGGGA GCAACCTGTACCACAGGGAGAGAGGCCTAA GGACAGGAAAGGAGCTGACCCAGAACTGAA AAGGCACACACCATTTCTGCCAGCACTCCC	323 783	C	--
IM000450	CATGTCCTACAGTGGACATTTCTAAATTTCCC TTCTTTTTCAGTTTTCTCGCCATATTTACAGT CCTAAAGTGTGTATCTCTCATTTTCCGTTATTT TCAGGTATCTCGCCATATTCAGTTCCTACAG TGTGCATTTCTCATTCTTCACGTTTTTCAGTG ATTTTCGTCATTTATCAAGTCGTCAAGTGAATT TTTTTCATTTTCTCTGATTTTCAGTTTTCTCGC C	324 784	R	--
IM000451	CATGTTGCCTCAAGACAGATCTCCACTTTAAA GACATACCTAAAGGCCTGGAAGCTTAGTCAA TTAAGCTTTCTGCCAGACACTCCTCCCTG AAAAAGGTATTTAACCTCAGGCCACCCCTGA GAAGTGGGGTATGATTTTACTCATCCACTTTC	325 785	R	--
IM000452	CATGGTTTCTATTACTGTGTTGAAGCACCCCTG ACCAAAGCCAATTGGGGGACGAAAGGGTTTA TTTGGCTTAAACTTCCAAATCAGTGTTTATCA TTAAAGGAAGTCAGGGTAG	326 786	R	--
IM000453	GCAAGTGTGACAGCGGCTCTCAGGGAGATACA CATAGCTTTATTGGATAACTGCAGCTTGAAGA CATG	327 787	D	--
IM000454	CATGTACCTATGTGTGTGAACATTTGCCTAT TTTCACACAGTTAAGAAAGCATCGTTATGAAA ATCATTACAACCTTCCAGATAAACAGATCCAC TCAGCCACAGAT	328 788	D	--
IM000455	GCCCTTCTCTCTGAACTTTTCAGTTCCTGGAT AAAGTCAGTGTTCCACCTCTATACCTGACTAG TTTTCTAAATTCTGAGTCAAGCATATTTTAT G	329 789	D	--
IM000456	GACCTCGTGGGCGGGCCTGAGGAGACAGTG CAGATGAGGTGTCAGTAAGGAGGATGCAAGC AAGAAAGATGCAGGAGATGATGGAGAAGCTG AAGAAGGCACTGAAGAAGGCACAGGGAAGA AGAGTGCATG	330 790	D	--
IM000457	CTTGCCGTTGAGAGCGTCCAGATCCCCTGAC TTGAGTGGGTCCACCTTGTTTGGTTTGGTTC GCAGTGTGCGCTGTGGAGCCCCAGGCCTTG CATG	331 791	C	--
IM000458	TTCTTATCCACTGAGCCACACTGCTAATACTG TGATGTCTTTTTTAAGACTCACCATG	332 792	D	--
IM000459	GGGTTCAACACATTTTGGAGATTGATCAAAA TTAAACATG	333 793	D	--
IM000460	CATGAAGGAGAGTCTGAGGCTACATCCACCA	334 794	C	--

	GGCTCTATGATCTCCCTCTGCTGCATCCAGG ACATTCTCCTTCTGGATGAAGATGATGCTGG CGCTGGCGCTGGCGCTGACGCTGATGCTGC TCGCTTCTGCGTCCT			
IM000461	CCTTGTCCCTCAAATTACAAAACCTCCC TAGGGTCTTTTCTCTGGGCTACAAAA TTCTGCAAATGGACTCAGGAGGAAT CAATGTGGAAATTTCACTTTGCCTTC CCAATCAGCAAAATAATGTTTGCCAA AATCGTTAGATTTCTTTCCCCTAAGT AGGCTACTGCCGACTTGAAAGCAGT GGTTCAGAACCCGAGCCCAGGGG CTGCCACTTCCTATGCATG	335 795	B	AI4269 08
IM000462	CCCTTGTCCCTCAAATTACAAAACCTCC TTAGGGTTTTTTTTTTGGCTNCAAAAT TTTNCAAAGGGCTTCAGGAGGAATA ATGGTGGGAAATTTACTTTTGCTTTC CAATCAACAAAAAATGGTTGGCCAA ATCGGTAGAATTCTTTCCCTAAATAA GCTACTGCCGACTTGAAAGCAGTGG GTTCAGAACCCGACCCAAGGGCTGC CCTTTCTATGCATG	336 796	D	--
IM000463	CATGTATCTTAAGAACAGAGCCAGTGCTCTC CCTCTCCCACTTGAT	337 797	D	--
IM000464	CATGCAGANTAAAGTACATATATGAAAAAAT AAAAATAAATCTTT	338 798	D	--
IM000465	GTGCTCTCCCTTGCCTCTCCTCTCCT GAGTTTCTCTGTAGGTGTAAGGGCT GGAGGTGGGCCCAAGAACCAGAGAT CAGAGGAGGGAACTTCCGGAGCAGA GGCCCTGGGAGCAGTGTTAAGCAGG CTTTGGCCAGGTCTGGAGGTGTCCA GGCAGGGAGGTGGAGCTGGAAGAG ACCAATTAGTCAAACGGCTGCAATTG GCCATTTGGAAGCAATTAACAGGGT CTCCATTACCATATTATGCCCTCCA CCCCCTCCACACTCTACTAGGCTCT GCTCTGTATGGAAGGGGGAAGGTGG AGGCTCANCTCAAGCCAGGGAGACT ACAATGGAGGCCCAAGTGCTCGCCAG GATGCACACACTCAGGCACCCTCCG TGTGAGGAGGGGAGGGCAGGGCAG CATCTGAAGCAACCTGTCATTACAG CCTGANAGANGGTGGGAACAANGGC TTNCAAAGCCAAGAANGCANGTGGN TAGAAATGCANGAAAACCTCTCTGGT AAGAAAGGCTGAANGAAGCAGCTAG GGTTGTAAACAAGANCAT	339 799	K	<i>Fgf3/Fg f4</i>
IM000466	CTCCCTCTCCCTCTAGCTGGCCTAGCAGGGG CCAATACAACCTGCAGGGAATCAAGGAAGAGC	340 800	B	AI5500

	CTTTTCCTGAACTGTCCTGGATGCCCCAGTC CAACAGCAACTCCCACCTTGCCTGGCTTGGT TTGCTCCACTGTCCTGAAGGCACAGTGTGAT ATCCCAGACCTCCAGCGAGACAGCCCAACCT GCAAGCCCTGATGGGAGGGGTGGCCTGAGA CAACAGTACCTACATG			57
IM000467	CATGGACTCCAGGGTCAGGGTGTAAAGAAAA GGTGGAGCCTGCTAGGTGTGGTGACACACA CCTTTAACCCAGAACTCAGAAAGCTGAGGC AGGTGACTAGCCAGGAGTTCAAGGTCATCTA GTTTCATCAGATCTATAGAGTGAACAGCCAG GCTACATTTGAGATC	341 801	K	<i>Fgf3/Fg f4</i>
IM000468	GCTCAACACTTAAAAGCGCCTGCAGAGGGGT GGGGGTTTAATTCCCAGCACACATAGTGG CTCAGGGAATCTGAAGCCCTCTTCTGGCCAC TGCCTGAACTGCATG	342 802	D	--
IM000469	GTGGGAAGCTATACGAAAGTAAAACACACTC TAAGAAAGAGAACAGGCTGCCTGGGAGAGG GAGGTGCCAGGGGCTTAGACAGGAAGGTAG TTTTCAAAAAGTAAAAGTAAAGCTATCTGAA TGAATGATACAAAATAAAGAAAGACACAAGAA TTTCCAGTCACCTGAGATATCTCACACTCCTG TTCTTTCAACCTTCTAGCTGAAAGGAGAAAGA GCCATG	343 803	D	--
IM000470	CATGGAAGGAGTTACAGAGACAATGTTTGA GCTGAGACGAAAGGATGGACCATCTAGAGAC TGCCATATCCAGGGATCCATCTTATAATCAGC CTCCAAACCCTGACACCATTGCATACACCAG CAAGATTTTGCTGAAAGGACCCTGATATAGCT GTCTCTTGAGGCTATGCTGGGGCCTAGCA AACACAGT	344 804	R	--
IM000471	CATGCTTAGATTGACCGCAATATGTGTGGTA CTCTTCAGACTTTTAAAGATTTGCTGAATATC CTATTCCCCTTAAATTGTGATCACCTAGCTA GATCTAATCTTAGATCTCGAAAGTTCTACAAT TTGCCTCAATTTGATTACTGTTTTCTCCTTG AAGAC	345 805	D	--
IM000472	CTTGCCTTGGAAGTGAGGGGTCTAATGAA GGTTGCAAGCCTGTCCACCCAGGGCCCTGC TAAAGAAGGAATGGTCCCCAGCCTGTTTTGT CCCCTCTGTGGCTTCTAGTTCTGGACACTG AGCCAGTCTGGGCAGCAGGCAATTCACACTG TGAATTTCTGTGGAAAGCATTTTGGGGGTTCT GAAAGCCCTGTACATTCTGTGTTAAGGACAG AGGGCCTCCTGCATG	346 806	K	<i>Fgf3/Fg f4</i>
IM000473	CATGGGGGCTATGTCCTAGGGTAGACACCCC CTTTATCCCTCACCTCCTTCCCTGTCTTAGCA GTGGTGTCCCCCACTGTGACTCTACTGCATC TGGGAGCTGTCTCCCGGGGACTTCCTCCT	347 807	K	<i>Fgf3/Fg f4</i>

	GCTGGAGTGAGTAGGTGGCTAGGGCGAAGC CTGTGTAAGAGGCAGGAGGTGTTTTGCACAA CTCCAAAGGGTGCAGATCCTGCTGGCTCCAG CTTCCCAGGGCCAGACCCCCAAATACCCTTC ACCCAGC			
IM000474	GTGTATGTTCTCTGGTGAAAGTGTTAACCAG CTCACTCCGTGAAGAGCACGCTGCTTTCAGA TCAGTGTTCAAGTCTTGAATAATTGGTTTTT AGAATCATAAAATTGCAGTCCTTTACAAAGGA CTGGAAGTGACTCATG	348 808	D	--
IM000475	CATGTGAATTCTCTATTTGCAATGTGCTTGGT TCATACTTCCATACTCTACCCAGAGCCTGTTA GAAAAATCACTCTTCCCCACCCTATTCTTCAC CAGTCAATATGTATCTAGTATTCTAACTTCC TCCCTCCTAAGGCAGTGGGGAAG	349 809	D	--
IM000476	CATGTGTACTCTCACCATCAGAATTATGAGCA ACCCACAATTTCTTCACATTTATAACTGACCC AGTCTGAGGTATTGTGCCTTTAGCAACAGAA ACTGAACTCAAACAATCGGCACAC	350 810	C	--
IM000477	CCATATCAGACCAACCTTCCCACACAACAGT AGGCCACCAGGTGGGGGCAAAGTCTTGGGT AAGGTTCTTGGCACTGTAATTTTGAATCCCAA TAATAATGACTGTGTTATTTGCTCATG	351 811	D	--
IM000478	TAAACCTTTAGGGAGCTGATAAAATCTATC AAAACAACACTCTGTCTCTCGTATCCAGCCAT CCATG	352 812	C	--
IM000479	TCTGCCAGCCTTTGCTTCCCTCCCTGGTAAC AGGATGCTAATTAGAATTCATG	353 813	B	AA1177 84
IM000480	CATGTAAAAAAAACCTTCATTAACAA CTACAACAAAGCAGAGACCTTGGCC CTTGGATTGGGGCCCCCTCTGAGAGC TATAGGCTGGGATACTGG	354 814	D	--
IM000481	GTGCGTGATAACCAGGCTGGCAGTGCCCTCT GCATCCACATTGGGAACAGCAGCCTGATAC TCCAAGGCTGCCATG	355 815	D	--
IM000482	ATGTCAACATTGAGTCCAGTAAGGACATCGT ATATGCTGGTCATTATTATAGCTCTAAGGGT CATACATGAGACAGACCACCCCTTACCCCC TCCCCCGTCTGGGCTAAAAGCAGACACACTG GGTTGGTGAGAGAGCAGCAG	356 816	K	Wnt1
IM000483	CATGAGACAGACCACCCCTTACCCCTCCC CCGTCTGGGCTAAAAGCAGACACACTGGGTT GGTGAGAGAGCAGCAG	357 817	K	Wnt1
IM000484	CATGAGAAAAATTTGTCTCTAATTCTCTTTGTT GAATTTTGTGTGGTTTTGATATCAGGTGATT GTGGCCTCATACAATGAATGTGG	358 818	R	--

IM000485	CCAGTGAAGTAAACCCAGCAGGACCCTTTAC AAAGCCAGGACATG	350 <u>819</u>	D	--
IM000486	TCGGGGGAAAGTTATTTTATACCTTCCCCT CTGGATTAAGGGAGGGTAGGAAAGGATTGGA TGAAGCTAGAGACAGAGTGGCAGGAAGGTG GTAGACCTGAAATTGTCAGACAACCACTTATC GTTGGGAAGGGTATAAGGTGACCACAGCACT AGCAGACTGTTCTGGACGTAGTAAGGAGTTC CTGCAGGGGAGGAGTGGGTCAGCCTTTGAA TCCCATATGGTGGTTCACAAGTCAGCCTACA TG	340 <u>820</u>	D	--
IM000487	CATGTGTTTTTAGCAACTGTGCTCATTTTCTG CTGCTGCTAGGAATAAAATCAAATCTAGTANA ATTGCTTTAATACAAAGTTATTGTCATCCATCT CTGAAGATCTGAAGTATTGCTGGGGGGTCTC CAACTACCCACC	341 <u>821</u>	D	--
IM000488	CAAGGGCCTCTCCTCCCACTGATGGTCGACC AGGCCATCCTCTGCTACATATGCAGCTAGAG ACACAGCTCTGGGGGGGGGGTACTGGTTAG TTCATATTGTTGTCCCTCCTATAGGGTTGCAG ACCACTTTAGGTCCCTGGGTACTTTCTCTAGC TCCTTCATTAGGGGCCCTGTGTTCCATCCAAT AGATGACTGTGAGCTTCTTATAAGCATAAACT TCACTTACCACATG	342 <u>822</u>	R	--
IM000489	CATGGTGTTAGCCTCCAGGCAGGAAGCATAC CAGAGGAGAACTCCACAGGGAAGCCTTTGTT TTCTGCTGTTAAAAACAAAGTATGATGGGGCT TAGAAGAGGCTTTAAGAGGTCCTCTGGAGAA AAGAATCTATTTCCATT	343 <u>823</u>	D	--
IM000490	CATGAGAGGTTTTTAAGTCCCTGAAAGACCATC ATACCTAGAGTCTATACAACAAATAAACTTGG AATACAGTGAAGCTAGTAAAAATAACTTCCTG AGCTTATGG	344 <u>824</u>	D	--
IM000491	CACAGTCAGGAAGCAGAAAGATGAACGTTGA CTCTCAGCTCTCCTTCTCCCTTTAGTTCTATG GAGGTCTCCAGCCCATG	345 <u>825</u>	K	<i>Fgf3/Fg f4</i>
IM000492	CATGATAAAAGTCTTGAAAAGATCAAGAATTC AAGGCCCATAAATAAACATAGTACAAGCAATA TACAGCAAACACAGTAGCCAACATCAAATAA ATAGAGAGAACTTGAAACAATCCCACTAAAA TCAGGGACTAGACAAAGTTGCCCACTCTCTC TTTAACTGTTCAATAGAGTACTCAAAATCCTA GC	346 <u>826</u>	R	--
IM000493	CATGGTAGCTTTCTAGTGAGGTCTCT TCC	347 <u>827</u>	D	--
IM000494	AGTACCCTTAGCCAATAAACCATCCCTCTAGT CCCTGTTTGTTTTGTTTTTTTTTAAAGACAGG	348 <u>828</u>	K	<i>Fgf3/Fg f4</i>

	GTCTCACCATG			
IM000495	CATGAGCTAGGCCATCTGCAAGCTGGTCTCG TCTTGACCAGGAGTACACAGAAGCCTGGCTC AGGACTTGGTAAC	349 829	D	--
IM000496	GTTGTTTATGCAGATCTCTCAGCGTTAGCATT CTATGGGATTCTTTGGAAAGACCTTTTCAGTT ATCTTCCATTTCTGAGGCTGTTTCTAGGCAAC GGAGTGGTACCTTCCTTTAATCTTCCCCTGAC CTTTTCTGCCTATGAAGATGTTGACTAGTGAG CCCGTGGGGATGTGTATTATCTGTTACATTTA TTTATGGCTTGGTAGCGACTCCTTGGTTGTTG TTCAGCTTTTCATG	350 830	D	--
IM000497	CATGCCTCCCTCAGCCTCCTCCCAC CCCTTCCTGTCCTGCCTCCTCATCAC TGTGTAAATAATTTGCACCGAAATGT GGCCGCAGAGCCACGCGTTTCGGTTA TGTAATAAAACTATTTATTGTGCTG GGTTC	351 831	K	<i>Wnt1</i>
IM000498	TCTAAGTCCAGTCTTTCACACACACTGACTTT GGTCATCTGTAATCACAACATG	352 832	D	--
IM000499	CATGCACACAAACTGGCCCTGAACCTTTGAC TTCCAGGCCTCTGCCTCTCTGCGCGCACACA CACACTCGCACTCCTGTATATGAAGCGTATAT GTGTTTCTCTGGGAACTGTTTTATCAGGTGA AG	353 833	K	<i>Fgf3/Fgf4</i>
IM000500	GGGCTGAAGGAAAATGTTGTGTGCAT CTTTGTGGCATG	354 834	D	--
IM000501	CATGTACCACTTTTGCTAATCCCCTA ACCGCCCTTGGTAAGCATCTAAAG TGATATATCTCTTGGTCTACTGAAGT TCTGCCCTGTCTCCATCGGGGATTTC TCGGGAGGCTAAAATTATAGACTATT TGTGAAAG	355 835	D	--
IM000502	CATGTCCTTATGATATGGAAAAA	356 836	D	--
IM000503	CATGTGCCAAGAGCCATTACAGGCT CAGACTAACATCTGCCTGTAAACAAC GGTTGCTAAGTTTCCAGGGAAGCGT AAG	357 837	D	--
IM000504	CCAGATGACCTTGAATCAGAGATCTCCTTG CCTTAGCCTCCTGGGATTCATAGCCGCTATG CCTCAAGATCTCCATG	358 838	R	--
IM000505	CATGTAGTTTGCAAACAAGACATCCCTGGTAT ATCCAGAACCTGAGCTATGC	359 839	D	--
IM000506	GGATATAGTGTCAAACAGTCTGATGTATTCAT AGGTTTGTATCCATAGTTATCAAATCTCTCAT G	360 840	D	--

IM000507	CATGTACCACACACAGACTTGGTAATAAGTTA GATGATAATTACAAAAGCAACAAATAAAACCA ACAAAACAAAACAAAGCTTGGTAATA	361 841	D	--
IM000508	GTTAGGAGCACGAACTGCTCTTTCAGAGGAC CTGGGTTTAATTCCCAACACTCACATG	362 842	R	--
IM000509	CATGGTCAATGATAAACATTCCAAAACACCAA AACCATCCTCTCTGTACAGGCTATGATGATTC AACTGCTGCCCTTCCTCATTTCTTGTTCCTCAA CTCCTACTGAATATTTCTCTGCAT	363 843	D	--
IM000510	CATGATAGAAGACCACGTCTGGGATGGGGTA AGGGTTTCTCAGAGTACCTTGCCCTGGGGCC ACATCCTAAATCTACAACAAAGCTGACCCTA	364 844	D	--
IM000511	CAAGTTTTTGTAAAGGGAGCTAAGAAAGGCAT TGTTGGTTAGGTTGGAAGAGGGGGCAGGA CCTGGCTCTCGCTTCAGCCCACTCCCTCTG CCCCCAGCCTCAAACACTTTTACCCTAGCA TAGCAGAAACATG	365 845	D	--
IM000512	CATGAACCTCAGTGGGCAGATGAAGAGTTTTT GTGTGAACCTGGGGCTTGGCCCTTATCATCCT GTGTGTTCTCCTGGTGACCCTCAAGCTTGGC TGCAATGATCCCCACTTACAGAT	366 846	K	<i>Fgf3/Fg f4</i>
IM000513	GTTTATTACTCCAATGATTCGCACAGCCGGG TTGCAAGTCTAAGGCAGGCTGTCTGCCTTCC TGGAGGTAATTACCCACCTCCCCCTCTGGG GGAGCTCCACTTGCCATG	367 847	R	--
IM000514	CATGATTTTCAGTTTTCTTGCCATATTCACG TTCTACAGTAGACATTTCTAAATTTTCCAATT TTTCAGTTTTCTCGCCATATTTACGTCCTA AAGTGTGAATTTCTCATTTTCCGTGATTTTCA GTTTTCTCGCCATATTCAGGTC	368 848	R	--
IM000515	GTAACCACTCATTTACCTGCCCCAATGATGTC TGGGCCAAGGCACTTTTAAATTCATATCTACT GTGACTATAGGTGCCCATG	369 849	D	--
IM000516	CATGACACTGCTCACTGTTGCTCTCTAACCTT GGTCCAG	370 850	D	--
IM000517	GNGCTTGGCAGAGTAGAGAACTCTTTGGGA AACTTGGTTCAGATCCAGACATG	371 851	C	--
IM000518	CACCTCTGCCTCAGTTTCCCTGATTA TCAACAAGTGCTCATG	372 852	D	--
IM000519	CATGTAACCTCAAGAAAGTCTAGTAGGCGTAG TGGTAAATGCCTTTGATCCCAGCACTTGGGA GGTAGAGGCAGGTGGGATCTCTACAAATTCA AGACTGGTCTGGTCTATATAGTGAGTTCCAG GCCAACCTTCACATTGAAATTCATCTCAAAAC AATAAAAAATAGAGGAAGATATAGTCAGGCAC	373 853	R	--

IM000520	GAAGACATTCATTTTTTTCTTGGGAGGGGATA GAATCCAAGGCTCCAAAGCAGAGTTCATG	374 854	D	--
IM000521	GACCACGCTGGCCTCGAACTCAGAAATCTGC CTGCCTCTGCCTCCCAAGTGCTGGGATTAAA GGCTGTGCCACCACTGTGCTTACTGATCTCT TTGATGTCCCAGTTATAGCTCTTGGGTCCCC ACCCATTTGTAGGGGGACCCAGGACACCTCA GAGCTCTCCCAAGTCTAAAAAGGGCAGGGTT CCTGGCTCCCTTAATGCCTTATCAAGCACAA CAGAACTCAGGGGCAGAAAATGTTCCAGGA AGAAGTTAGCTGTGGGGAGAGTCATG	375 855	R	--
IM000522	CATTTTTCTTTATAGCTGAGTGTTATTCCACT GCAAAAATTTGAATATTCCACTATTCTGTTGA TGAATGTCTAGGCTGGTCACGTTCTCTTGCC TTTGTGAATGGAGCAGCAATAAACATAAGTG GGCATG	376 856	D	--
IM000523	CTCCATTGGGCCGAGTGAAGCTGTGGTTCAG AGAAACTCTATGGACAAGCTTGACTTCCAGA ACATTGACCTGGTCTCTGAGATCAACAAGCG TAGGAAAGCCATG	377 857	D	--
IM000524	CATGGGAAAGTAATCCGTGGCTAACACAAAG GGGAAATAAAGTAATATT	378 858	D	--
IM000525	CATGTAGGACCCTGAATGCCAGCAATGAACA ATACCAGCTTGGTTTTCCGACTCTTGCTTTCT CCTCCCTCCACTACTAACTAGCCTCACCGTT GCATCTTGTGACTCAGAGGTCTTGTTTCCAG GGCTTCCTTCCTTCCAGTGTTCTTCTAATGCA TCTAAAGTGAAGGGGTGG	379 859	D	--
IM000526	CATGCAAAGCCTCTGCAGGGCCGACAGCAA GGAAGGCCCTTCTAGATCTCCAGCACTCTGT CAAAAGCCATCACTCGGCAGGCAGGCAACCA CAATGTAGGGAAGACCTGTAAAGCCTTCAGA GAGGAACAGCTGGCAGCCCCTGGGTCCTC AGAGTGGCCAACAGCTACTCTTGTTGGAGACA GCAGGAGGAGGCCTAGACTATAGAAGGATG GAGGAC	380 860	D	--
IM000527	CATGCACACAAACTGGCCCTGAACTTTTGAC TTCCAGGCCTCTGCCTCTCTGCGCTCACACA CACACTCGCACTCCTGTATATGAAGCGTATAT GTGTTTCTCTGGG	381 861	K	<i>Fgf3/Fg f4</i>
IM000528	CATGAAACATTATTTNTTTTGGAAAGT CTGCAGGTAAACTTAAATAGGTAA	382 862	R	--
IM000529	AGCAAGAACAAAGGAAGTACTTCACCTGATA AAAACAGTTCCAGAGAAACACATATACGCTT CATATACAGGAGTGCGAGTGTGTGTGTGAGC GCAGAGAGGCAGAGGCCTGGAAGTCAAAAG TTCAGGGCCAGTTTGTGTGCATG	383 863	K	<i>Fgf3/Fg f4</i>

IM000530	GATTTTATTTTCCTTAGCATCCTGATTGGAG ATGCCTGGGTGCACATG	384 <u>864</u>	K	<i>Fgf3/Fg f4</i>
IM000531	CATGTAGAGACTGCCATATCCAGGGATCCAC CCCATAATCAGCATCCAAACACTGACACCATT GCATACACTAGCAAGATTTTATTGAAAGGACG CAGATGTAG	385 <u>865</u>	R	--
IM000532	GACCTGTACCCTACCCTCTGATGGAGGCCAT CTATTTGCCTGTCCCCAGGAGTCCCCAACT GCTCAAAGAACAGACTGTGGGCTCTGGAAAG CTAGCAGGTGACCCCGGGGGATGTTCTGAG CAGTGCCTTACTGAAGTTTATCCAGGCCCTA GGGTCCCCTCAACTGCTCACACAGCCTAGGG TGGGTCTCTTGAGGAGTCACTTGCACTTCT GTTGCTTCCCAAGAGACCCAGGGAAGG AAGGAAGGCCATG	386 <u>866</u>	D	--
IM000533	ATCTCACTCGTAAATGAACAAAGGGACTGC AGAGATGGCTCTGAGCTTTTAAGACCATAGC CTGCTTTTCCAGAGAGCCCAGGCTTCATTTT CCAGCCCACATATGGCAGTTCACAACCATCT ACAACTCTAGTTCCTGGGGATCTCACACTTTT GTCTTCTGTGGGCACTGCGCAATGTGCACA GAAATACACGCAAGGAAACACCCATG	387 <u>867</u>	K	<i>Fgf3/Fg f4</i>
IM000534	AAGAAACACTCTTAGCTGGGCCTGGAAGTGC ACATG	388 <u>868</u>	D	--
IM000535	CTAAAGCAGATTATTATACTTATTCTACTGAC CATAATGCAACCACTATTATATAAACAGAACA TACTATAAAGTGAATAACATTAGGATACAAAA TGTATAAAAGGGGAGAGAGGATAACCATTTGT GAAGTATGTTTAAATAAAATGTTTGGGATTG AGGAAATTAATAAATTAGTTACCCTTTTTGCTT TGGGGAAAGAAAGGCAGCATG	389 <u>869</u>	D	--
IM000536	CAGCCCCAAACCCATCAGCCTGAGACTGATG CACAGGAGGCAGGCCAGTTAGTTATTCTCTG GGCCCCTCTATTTTGCTTCTGTAGGTTAATC CCACCGCTCCAGTGCTGGAAAGTGCAAGCA TTGTGGGAAGTTAAAACGTGCCACCATG	390 <u>870</u>	D	--
IM000537	CATGGACAATGCACCCCTCAAGCAGTGTCTT CCATACAGACAAGCATATTTATTTCTATACA GACAGCAACTTTGCTGAGGTGTAAGG	391 <u>871</u>	K	<i>Fgf3/Fg f4</i>
IM000538	GGATGAAGAAGCCCAAGGTATTAGGTCAGTC TTGCTCTGACTTCTCACAGTAAAAATACAACT CCCAGGGACTAAAATGACACAGAACAGCTTA GCCTCTGGACATTGCTTTTGGATTGCAAAGT GATAAGTGAAAAAGTAATAAGTCTATCTACAT TGGAAAACATTTGGTAACTTCATTAAACACA CTTCCCCATG	392 <u>872</u>	D	--
IM000539	CATGTCCTACATTGGACATTTCTAAA	393 <u>873</u>	R	--

	TTTTCCATCTTTTTCAGTTTTCTCAC CATATTTACGTCCTAAAGTGTGTAT TTCTCACGTGTATTCGTTGGTTGTTG GTTTAGTTCCTGGGAGCTCTGGAAAT CTGATTATT			
IM000540	TGGAAATGAGAAACATCCACTTGACGACTT GAAAAATGACGAAATCACTAAAAACGTGAAA AATGAGAAATGCACACTGAGGGACCTGGAAT ATGGCGAGAAAACGAAAATCACGGAAAATG AGAAATACACACTTTAGGACGTGTAATATGTC GAGGAAAACGAAAAGGGTGGAGAATTTAGA AATGTCCACTGTAGGACGTGGAATATGGCAA GAAAACGAAAATCATG	394 874	R	--
IM000541	TGACATACAGAAAGAACACAAATACCTGTAG CTGCTGTGACAGGACCAACCATTCTAAATATC AAAGCAGCTGTTGACACCTAAGGACTGGTCT GACTGCTAGATCTAGGAGTTTCAACTTGCAAA AGCTGGCTTGATGCTCATG	395 875	C	--
IM000542	TTATATATATATATCGTTTTCTTACTCCTGA ATCAGTGACATG	396 876	D	--
IM000543	CATGTCAGCCCTCAGCTTTACACAGGTGTCA AAAAAAAAAAAAAAAACACTGACTGAGATCTTCC GTCTGCCATTAGCTGTTATTGTGTACATTAAG TAGAATCCACTGCTTAACCCAGGCTACTGGG CTCACCCAGTATTCAAGGAGGTGCCACAGG ACTCAAAGGATACAGAAGTTACATATTTAAAC CCAATCTCGTAGAGGATTGAGAGGAATAAG TTTGGTAGGGGCACAGATTGTAGTACCATTA AGCCCCCTGTTCCTCGTGGAGAACCCTAC TGTCAGCAAGGCGGGAAGGACCCAAATCAA GCAAATGAGACTTGTTCTGG	397 877	D	--
IM000544	CATGATANATCCCTTTTTGTGAGCAT TCCATAGCCTCAGTAATAGTGTCTGA CCTTGGGACCACGCTGTATCCCACT NTGGGACCTTCTTTTCNTCAGGCTAC TCTCCATTTCCATTNCTGTAATTCTTT CAACAGAAACATTTATGGGTCANAG GTGTGACTGTGGGAGGACAACCCCA TCCCTCACTTGATGTCCTGTCTTCCT GCTGGAGGTGGGCTTTATAAGTTCC CTNCCCCTACTGNCCAGCATTTATC AAAGATCCCTCCCTAGGAATCCTGG GAACCTCTC	398 878	D	--
IM000545	GATAAGCTTATCTTGAACCTGAATGTATATGG AGAAGCAGAAACCTTGAAACAGCCCAACAGAA ACTGAAGAAGGATGAAGGTGGAACCTCTCAGC TGGAATATTATG	399 879	D	--
IM000546	CATGTTCCCAGCTGGGCAAGGCCTCGGGTTC CTCGGTGAAGAGTGTGGACCAGCCGATGAG	400 880	B	AI4132 88

	CCCTCCGACGTGTGGATGAAACGGCTGGCTT TTGTTTAGTTTTGTTTTAACCTCCCCAACGAG ACTTTGATCAGCTCCACCTCGAAAATGTTGCG GAAAGATGCGGAGAGCCTGAGGGACTGCGG GGCAGCAACGGGGCTCCGGCCTAGCCCCGCC CGCCGGCCCCCAGA			
IM000547	ACCAAGTGTTAATAATGTACTGATGGCTTCTG CCTGTGGCAGTACACTTGTCTCTACACATG	404 881	C	--
IM000548	CCTTACTGCAGAGATGACTCGGCCAACGGCT TCGAGCCCCCTGACCACTTCTCAGGTTTGGT TTTGTTAGTTTTTCTCACAGCAATGGGAAGC ATAATCAATACTTCCCAGAATGCGACCTG TGACAAGGCCAATGAGCAGACTCAAGGCTGG GCACATAAAAGCACCAAAAAAAAAAACTCCCT TGCAGTTATTGTTTCATG	402 882	D	--
IM000549	GACTGAGCCTGCCTGGGGCCGCTAG GGAAGGGGGGGTTGGACCCTCTGG TATTTGCAGTTACCACTGACAGGGTT TTTCCGAGATGCCAGTGTGAGGGTG TTCGGTGCTGACCCCCCAGGGACCG TGCAGCCCCGATGGCTGTCTCGGTC CTCTCANCTTTTCCGCCACCCCTGG GATATTTGAGGACTCANTCCCCGCAA CAGCTCTGACTGAGGTGAGCTCTGT GACCAGGGNCCCTGTCCCCGGTGT GNGTGTATTTGCATG	403 883	K	Wnt1
IM000550	CATGTAGAAGGCAGAGGACAACCTTCAGGGA TTATTTCTGCCCTTTCAC	404 884	C	--
IM000551	GTTCTCCATTCTGCTGCTTCTCCCTGATACA TTGAGTTACAGCAGCCCACGCGTACACACTC TCGCACATG	405 885	K	Wnt1
IM000552	CATGCCACCAACAAATAAGTAAGTAAAAAAGA AGGAAGGAAGGAAGGAAGAAAGAAAGAAA ACATTTTAAATCTGTAAT	406 886	D	--
IM000553	CGGAGCTTAGGTCTATCATTTAAAGATACAAC CAAATAGGCAGAATCATTTCTGAGGAGCCC ATTTTCTTTATCTCAGGTCTGCAGATTTCTC CCTGGTATTATCAGGGAGGAGCAGCAGCTGA GCTATCCTATCTCCTTTACTAATAGAAAAAAC GCCTTTAGGGCTTGAGCACAGGACCTGTATT TCAGGGGAATGTTGACAATCCATAACTCCAG GGTGGACTACTAAGCCCTGCAAGGTGAGTGA ACCCCGGCCGAGAATAAGGCCCATG	407 887	R	--
IM000554	CATGGCCTGAGAGTTGAAAGAGTATTGTAA GCAGGGGTTGTTCCAGAAAGTTTAGAATATA CAGACACTATACTCTATCCAGACTTCTTGGA CAGGGAGTTCAAATGTAGACTCTGAGCCCCG TCCTGGGGCAGCTTCTTCCACCTGCTTTGGG	408 888	D	--

	TAGAAGCAGGCAGACTCTGGGTAGACTCTGA TTCCAAGGCTAAGTAACCCCTGAACCCAGAA CAGTGTTTTT			
IM000555	CCAGATATCATACTGAGTTCGTAGGTGGTTTT AATTAATCACGGGCCCTGGCATG	409 <u>889</u>	D	--
IM000556	TTGGTGATCCAAACCCAAAGAGACAAATGCT GAATGTTCACTCTCATTTTCTGTTCTTAGCTC CAAATCTTCAGATATGAGTAAGCAACACATAA ATTATGAAGGGACCATACTGGGATGTAGGGG GCTTGCATG	410 <u>890</u>	D	--
IM000557	CATGAGCACTGCTCTAGGGACACCT CCCATCCCTTCCTAGCACCCCAAAT GCCCCTTCCCATCTCTCCTTCCAGAA GTTGGA	411 <u>891</u>	K	Wnt-3
IM000558	ATATAGCTGTCTCCTGAGGGCCTATGCCAGT GCCTGGCAAATACAGAAGTGGATGCTCACAA TCATCCATTGGACAGAGCACAGAGTCCCCAA TGAAGGAGCTAGAGAAAGTACCCAAGGAGCT GAAGGGGTCTGAAGCCCCATAGGAGGAACA TCAATATGAACCTAACCAAGTCCCCCAGAGTT CCTTAGAACTAAACCACCAATCAAAGAAAACA CATG	412 <u>892</u>	R	--
IM000559	CATGATAAGGTTAGAGTTTTGTGAGCCTCCTT AACCTTGCTCAGCAAGCGTTGGGCTCTTGGC AGCCGAGCTGCCATCTTTCTCATCCCCGATA GAGCCAGCCGCCCTTGTCTGTCTTGAATAA GTTAGAGGAGGCATTATAGAGCGGACCTAAA CATTTGCCTTGGAGCCTGAGGGATGGGGATT GGCTGAATGTGAAT	413 <u>893</u>	D	--
IM000560	CAGAACTGTGCTCTTTAGGAAGCCAGACGCT ATGCCTTAGGCCCTGTTCCCTCCAGACCTTG CTCTGTGCTACAGTGTAAAAGCGAAGATCAT G	414 <u>894</u>	D	--
IM000561	GAGAATTAGAAAAGAGATAACAAAGGCGAGA AAGAGAGGCGTGTGAGAGCATG	415 <u>895</u>	D	--
IM000562	GTTTCCAGATTGTCCTAGTAGCTGGGCTGCA GGAACAGCCAGCATG	416 <u>896</u>	C	--
IM000563	GGGGGTGGGGGTGGTAAGAGAAGATTAATTA GCCTAGCATATATAAGGTTTTGGATTCAATCT TCAACTCCACCCCTTAAAGAATAAATAACAA GTAGATAGATTATAGACAGACAGCTAGATGG ATAGACAGATAGCTACATAGATACATAGATAG ATGATAGATAATAGACAGACAGACAGATAAAT GATAGATAGATGATAGGAAGTCCAGTTAAC AAATGGAAATAAAAAAGACAAAAGTCCCCTTTG TCCATG	417 <u>897</u>	D	--
IM000564	GTATATGGAATATGGCAAGAAAAGTGAATATC	418 <u>898</u>	R	--

	ATG			
IM000565	CATGGTAAAGGTCAGGAGTACACCTGTGCTT CTGTGTTCTTCTGTGTTGGCTGACAGCTGGG CAGAAGTGAGTTCAGGAGGNCAACCCATACG ATGAGACAAGCCGGGGCAAAGTGGGATATGT GGACCGCAGCACATCAGAAGGGTGTGCCCCG ACATAAAC	419 899	B	AA1113 54
IM000566	CATGAAGTATATTATTAGAGGGGAAGTACTGTCT TACTGCTGAGCAGCGTGTGTTCTTCTACAGA GGATGTTTGTGTTCTGGAATTTAAAATTACTT AAAGTAATAGTGTCAATGAAACGTTGTCCGGT GACTTGCTTCTTTTAAATGATCACTGTTAGAC AGGGA	420 900	R	--
IM000567	AATAATCAGATTTCCAGAGCTCCCAG GAACTAAACCAACAACCAACGAATAC ACATG	421 901	R	--
IM000568	CATGATTTGATAGGGTTATTTGGTCTCTGGA ATCTAATTCTTGAGTTCTTTGTGTATATTGG ATATTAGCCCTCT	422 902	R	--
IM000569	GCAAATAGTCCTTTGTACCGAACTTCCACACA CTAATGTAGTGAATTATTTAAAATTTATTCCTT AATCTTTTTTTAAAGTCCAGACTCTATCCCC TCCTTGTCACCCTCTGATTGTTCCACATCCC ATACCTCCTTGCCTCATG	423 903	R	--
IM000570	TTCCATCTCTTGATTCTGTTGCTGATGCTCA CATCTATGTTTCCAGATTTCTTTCCTAGTGTTT CTATCTCCACTGTTGCCTCACTTTGGGTTTTT TTTATTGTGTCCACTTTCTTTTAGGTCTTG GATGGTTTTATTGAATTCATCACCTGTTTGG TTGTGTTTTCTGCAATTCCTTAAGGGATTTT GTGTTTCCTCTTTAATGTCTTCTACCTGTTTG GTTATGTTTTCTGTAATTCCTTAAGGGATTTT TGTGTTTCCTCTTTAATGTCTTCTACTTGTTA GCAGTGTTCTCCTGCATTTCTTTAAGTGAGTT ATTTAAGTCCTTCTTGATGTCCTCTACCATCA TCATG	424 904	C	--
IM000571	CATGAGTTTTCTACTTTTTTATAAAATTATATA AAGTCATTTAGTAGAACCTAGCTTTATTTAATT TTACCAATTAATATAAGGCCACTGATATTATT GACTTTTGTCACTACAAAATACAGCAATGAAA TAATCTTTCTTCTAGGCTCCTTCCTCATCAA CTAGTTCTTCAGCTCACATTAATACTTTTTCA AGTTGTAAGGGACCTCAGGGACAGGGGGC	425 905	D	--
IM000572	CATGAGCTTATAGTTTCAGTAAGAGAGCATAG ATAGAATATAGGTGCCTGTGCGCTGGCTCTT TTGGTTGATTTAAATCCTTTATCTCTGAGAA GTCGGAACTGTTGGCAACAGACAATATGGTA GCC	426 906	D	--

IM000573	CTGACACAGGTATGCCCAGTCCATAGTGTGC AGAGCACAGATGGCCAAGGATAACTAGGAAT GAGACCTACTTAACCCAACTCCAAACATTAT GAAACTTTAAAAAATGACTTCAGTTGAACTT TGCAGGTAACCACATCATG	427 907	D	--
IM000574	ATTGTGTCCTTTTAACATTCTTGCTTTAGTAGA ACATCCTCTGACCCGTATCTGATTCAGTGAAA AATTCCTTCACGAGTCTGCCTTAGCAAAACAT CCTTTCACCTGTGTCTGCTTCAGGAAAACAC CCCTTCACATG	428 908	R	--
IM000575	CATGTTGGTAACAGATACAACAAGCAGACTTA AACTAATAAGAAAAACAGCTATGATTAATATGT TTATAACTTAGCTGAAGAGAAATGTATGGAGCT TTGAAGTTAATCTTTTCATATACACAGGAATG CCTTCAAAAAGCATTGCAGCAGATTTCAAAG GATTAAACTCAT	429 909	D	--
IM000576	CATGTGGCGAACCAGCATCACTTTTGCTCTTT CCTTACTAACCCAGGACATCCATCATTATTTT AATAGCATCCACCCTAGTAGATATAAGGTGAT ACCTTATTGTGATTTTCATTTGCCTTTCTCTGAA GATCACTAACAATCAAAATCTGGTTCATTTTA TTTATGAATTCTCATTTGTCTTTTGCTAAATAT ATGTTCAACAATTCTTTTCAATTTAAAAGCAAAT TGTTTTGTTAATAATGAGCTAACTTTTCATACA TTGAAG	430 910	D	--
IM000577	TTGCTGTGGGCCTAATTCAAGGCTG ATAGATCACCACAGAAGGACACTGTT TTCCTCCGGGCAGCAGGAAGTACAG GGTAGGGACTCTAGAATCACTGCCC TAGGGCATG	431 911	B	AI6639 69
IM000578	GTA CTG AAG TTT TAG CTAGAGCAAAAAGACA ATGGAAGGAGATCAAGGGAATACAAAGTGGG AAAGAAGTCAGAGTATCATTATGTCCAGGTG ATATGATAGTATACATAAATGACCCTATAGAT TACACCTAAGACCTCTACAGTGGATAAATACT AAAATATTTACTACACAGAAATCACCCCATG	432 912	R	--
IM000579	CATGCAAGGTATGAACTCACTAATAA GGGGATA	433 913	D	--
IM000580	CATGGTTCACACTCCATAATATCTTGTCTCA CTAATTCCTCTAATCCCATATATACACCAAT AATTTAACAAGGGAATTTCTACATTGATTTGT AATAAGGGAGATACTGTGTGAACTTACCCAA CAAAAGTCTCCAATAGAAGTGTGGATACCAC AGGAAGTCTTGTGACAACCATTAATTTGGG TCTGATAAGAAGATAACCCTTTAAATATATAG ATTATGTAAAG	434 914	D	--
IM000581	CATGGGCTGGGGAAAGGCAGAGAGAAGAAC ATCTGGATTGTTCTAACTTTGCCTTTAAAT	435 915	D	--

	GAGACTTCAATAATACTTAGACGTACCAGCTT CTCACAGTCAGTTAAATGTGACACACACAC CTCTCAGCAGACTGAATGGGTGAG			
IM000582	AGAGATGGTTGGGATTTAAGTTACCA GGGTAGGGTCACCACAATCAACCCT TGATGCCTTTATAGGAAGAAACATG	436 <u>916</u>	D	--
IM000583	CATGGAAGTCTAAAAGACATTAGGTTCTGGAT GGAAGAAGAGAAAATTATCTTTAAGTTTTAGA AAAGGGATGATAAAACAAGTCTTAAATCTTCT CAATTTTGCCATAATTCATTTGAATTAATATTG GTAAATGCTTTGTGTGGTCCCATAAAGTTCAA TGTGTTATATCACTAAGTAGTTATTTGTAAAT TATAAATAGCCTCTAT	437 <u>917</u>	C	--
IM000584	CTTGTGAATTGTTTAACTGTTTTGAAAAAGTA GATGTTTTCTCTATTTATTTTGGGACAATTAT CAGAATTTGAAACAAACTGTGTATCTCTTATT TACTTTCTGCTTAACCCCATG	438 <u>918</u>	D	--
IM000585	CATGGTTGCTATATTCATTAACACAAATCATT AAAATCCTTAATGTAAATGGGCACATTTTCA AAATTAATAATATGAAAACCAATAAAGATAG AAAATTTAGGAAAAAAATAATCCAAGCAAGA TGTTAACATCCAACCACAGCAGCATATTAGCA GCAGGACAAAAATAAGGACAACAACCAAGAA AGGGATTGTGGTTAATGTATGCCTCATTGGA AGGGATAATAGGATGTAAAGTGTGACAATA AAGAGAAAAAATCTCTTTTAAATGTAAGTT AAAATAATAAAATAATTTAAAAATGGTGTTT TCAGGGCTGGATAATATTACTAACAAAACCAG GGAATTATTAATAAAAAATCTCTTATCAGTTAT	439 <u>919</u>	D	--
IM000586	AACAAGTTTTAATGGGGCATAGTGGATCAC ATTTGTGATCCCAGCACTTGAAGGTAGAAA TAGGTAAATTAAGAGTTCAAGGTCATTTCTCA GTTATGTAGTTGTACATTTCTAGCGATGTAGT TGAGTTCAAGGCCATG	440 <u>920</u>	D	--
IM000587	GTCTCCAATGTGCATTTCTCATTTTTACGT TTTTCAGGGTTTCTCGCCATATCCATG	441 <u>921</u>	R	--
IM000588	AATTGCATTGAATCTGTGGATTTCTATTAACA AGATGGCCATTTTTTCTATGTTAATCGTAC TGATCCATCAGGATGGCAGTCTTCCATCTTC TGATATCGGCCTCAATTTCTTTCAGGGGC TTGAAGTTATCGCCATG	442 <u>922</u>	R	--
IM000589	GGCTAGGTACTCTAAACCTTCTCTGCTATC CTAGGCCCAATAGAAAAAAGTGGCCCATG	443 <u>923</u>	D	--
IM000590	AATAATACTTTCACTGTACTTTAAATATTATC TCCTATCTCACTCTAATACTTCTGTGAAAGAA GCAATATCGTCTCTTTGTAGATAAAAAATGGCT GAGAAGGGCACCTTCAAGACACTAAGTGACT	444 <u>924</u>	D	--

	AACTCAGACTCAGAAGTTCAGAGACCATG			
IM000591	CATGCTCTACTATGTTACAGCAGTCTTATTT ATAACTTCCAGATACTGGAAGCAACTCAGAT GTTCTCAATGTAAGAATGGATACAGAAAAA TATGGTACATTTACACAATGGGGTACAACCTCA GCTATTAAGAACAATGAC	445 925	R	--
IM000592	AAAACCCAAGAACAATTAAGCTGTAG TTCCCAAGTGTAATTATATTATGGTT GTTTCTGCTTGCTTTATATCCCTATAT ACAATTTATGATTCAAGTATTAGTGG GAATAGACTAATGGCATG	446 926	C	--
IM000593	CATGCCAAGCCTTCTGGTATCACCTAAAGG C	447 927	C	--
IM000594	CATGCTCTTCTCTGCTGTTCTTACTGAATTTT AATAAGAACAATCCACACAGCTCGAAAGCA CTGCTCAATTAAGAGATATTCCTACCAGGCAT CTTTGGAATCCTGCAAGCACCTCTTCTCTGTT TCCTGATGACCCTCAATTTGGTTGTGTCCAGA GGTTGGTGGGGAGGAGGGGAGGGGAAACG AAGCTTATTTTTTTTAATTGCAAGTTCAATTT TACAATGTTCTCGAT	448 928	D	--
IM000595	CATGCTAGGCAAATGCTCCACTGAATGAATTA CATTTCCAATCCTTTAGATGCATTTTAAAGAG AAAAGATTGAGTACTGAAGTTTGAATAGAAT ACAGGAATAAGGGACTAAACATATATATAGCC TTATATAGAGAAATATTAAGTAAGTAGTAACCTT TGCTTGTGTGTGTGTGTGTGTGTCACAC	449 929	D	--
IM000596	CATGCCATTAGTCTATTCCCCTAATACTTGA ATCATAAATTGTATATAGGGATATAAAGCAAG CAGAAACAACCATAATATAATTACACTTGGGA ACTACAGCTTAATTGTTCTTGGGTTTT	450 930	C	--
IM000597	CATGCACAGCTGGTGAGTGAGTTGTCTTCTG GTACAAAAATCTCCTCACAGGCACATTTACAA GTGCCTATATCTTTGCTAGCTTCAAGAACACA AAGAAGGGACACACAAAAGCTCTTCTGAGTC TCCTTCTCCTGCTGTTATTTTG	451 931	D	--
IM000598	ATCGTCAAAGTTAGCAAAATTATAAATGTGAA AGTCATG	452 932	D	--
IM000599	CATGAATTATGTTTGTTTTATTTCTTT TGTACATCATTCAATGCAGTAATCTA AAGTTTGGGGTCTTGGTCTTATATCT TGGAACCTTCAGTGACTTATTGTTCT AACG	453 933	D	--
IM000600	AGAGACAGTCACAAAAGGGGCCATTCTTGT TAAGAATGGGCCAGTGGAGAAGTTCGGGTGA GTGGAGTAGCCTGCCTCAGTTTCTCCTCTGTC TTCTGTAGTTAAATGTGTTAATGGTTAACATG	454 934	K	Fgf3/Fg f4

IM000601	CATGTAGCATTATCTTAGCCAGCAC	455 935	D	--
IM000602	CATGTACAGACTATGAACAGGAAATGTTTTG CAAATAACTCTGTGCATTAGAAATTTCTTCAG AAATATAACCATTTTGACAGTTGTAGGTTACA CTTTTAAAATTACAAAATCAATAAAATTGATCT ACAAACCGAGGCCTACAAAACCCCTTGCTGGA TATTGAAGACGGCATAATATTAAAG	456 936	D	--
IM000603	AATCCCACCACCCACAGGGTGGCTCCATAA CCATCTGTAAGTCCAGTCTCAGGGACTCCAA GGCCCTCTTTGGCTTGCAAGGGCTTGACACA CACACAGCGCACACATG	457 937	K	<i>Fgf3/Fgf4</i>
IM000604	CATGGTGAATGATTGTTTTGATGTGTTCTTGG ATTTGGTTTCGAGAATTTTATTGACTATTTGG CATTAACTCATAAGGGAAATTGGTCTGAAG TTCTTTCCTTGTTGAGTCTTTATGAGGGTATC AATATAATTGTGGATTCATAGAGCAAGTTAGA TTGTGTTCTTCTGTTTATATTTGTGGAATAT TTTGAAGAGTATTGGTATTAGATGTTCTTGA AGGTATGATAGAATTCTGAACTAAACCCATAT GGTCTGGATTTTTTTTGGTTGGAAGACCAAT GACTGCTTCTATTTCTTAGGTGTTATGGGAC TGTATAGATGGTTTATCTGAACCAGATTTAAC TTTGGTATTTGTTATCTGTTTAGAAAATTGCC CATTTTCATCCATATTTCCAGTTGTGTTGAGT ATAGGCTTTTGTAGTAGGATATAATGATTTT GAATTTCTCAGTATGTTTTCTTATATCTCCCT TTCCATTTCTGATTTTGTTAATGTGGATACTAT CTCTGTGCCTCTGTTAGTCTGGCTAAGGG TTTTCTATCTTGTTGATTTCTG	458 938	R	--
IM000605	CATGGGTAAACAGTGGGCCCTAAACTTGAAC TAGAAAACCTAAAGATGCTCATAGGGAAGAA GAAAAGAGCAGAAAGCTTAGCTTCTAGACAG GGGTAAGGCTTAGAGCTCAATAAAAAAGGAA CCCC	459 939	K	<i>Wnt1</i>
IM000606	CATGGCCTGTCTCAGTTTACTTCACAGCTGAA CAAGAGGCAGAGAGTGACAGGTAG	460 940	K	<i>Wnt1</i>
IM000607	CATGCTCGCCAGTCCCAGAACCTGG AAGGCTGAGGCAGGAGGATTAATAA GCCTTGGGGACACCAGGCTTGGTGG CACCGGTCGTAAATCCAGCACTGGG GAGTTAAGAAGCAAGTGAGTCACAT CTGTGAGTCTGAGGCTATCTTGGTCT ACGTAACCAGCTCTAGTATAGCCAG CCTGGGATACATAGTAACCAGTTCTA GTATAGCCAGCCTGGGATACACAGT AACCAGTTCTAGTATAGCCAGCCTG GGATACACC	461 941	D	--
IM000608	CATATGCGTATTCACATTTGTGTGGGAACGTC CTTGAGAAAAGCAGGAGCAGGAGTTACAGAC	462 942	R	--

	AGTTATAAGCTGCCTGACCTGGGTGCTGGGA AACACCTCAGGTCCTCTGGAAGAGCAGTAAG TCCCCTTAACCAATGAACCATCTATCCGTCCA GCCTACATTTAATTTGTTTTCTTATTTACTTTG TCTGCATG			
IM000609	CACACACACACACACACGGCTGGGGATCCAA CCCATCTCGTCCTTACACGTGCTCTACCATCA CGCCACACATTTCCAGCACNTTTATCTGAAGT GTTTCCTTTTATTTGTGCATG	463 943	K	<i>Wnt1</i>
IM000610	CATGCCTGGTGCCTGCAGAGGTCAGAAAGTG TTGGATGCCCTGGAATTAGAGTAACACATAG TTATAAGATGCTGCGTGGGTGCTGGGATTTG AACCTTGTCTCTGCAAGAGCAGCCAGTGC TCTTAACCACCGAGCCATCCCTCCAGCCCCT GATTACTCACTCTTCACGGCCTCAATCTTGTA AGGAATATTGAGGCTGCCAAGTGACGCAAGA GCACCTAGGAAGGCAGCCACATCGGTGGCA CTCTGGAAGCACTGCGAGGATGACTGCACAC ATTGCCGGTTGTC	464 944	K	<i>Notch1</i>
IM000611	CATGCTGGCCATTTATTTTGATTTAAGTTATA CTCTAGACCTTTGTAAATATTAGCCATTGCAT ATTACAGAAATTTCTTAGCAGAGATAGTCTCT CACTCTTAGTGATGAGCAAGCTGGAGCTCAG CATTATTCTCCAGCTAAGATACAGAATTACA GACGTTTATGACGGACACATCTTGGATGTAG TTACTTAGTCCAC	465 945	D	--
IM000612	CCCCCCCCGCCCTGCCAGACCGCAGCCCC AAGCACAGCATG	466 946	D	--
IM000613	CATGCCTCCCTCAGCCTCCTCCACCCCTTCC TGCCTGCCTCCTCATCACTGTGTAAATAATT TGCACCGAAATGTGGCCGAGAGCCACGCG TTCGGTTATGTAAATAAACTATTTATTGTGCT GGGTTCCAGCCTGGGTTGCAGAGACCACCC T	467 947	K	<i>Fgf3/Fgf4</i>
IM000614	CATGAATTCAATGGTGTGCTTGCTATAAATGC AAATAAACCATATATATCATATTACACTCAATT TTAAATATTTTTCCTAATATTAATAAAGGTGAT GGGGAACCTT	468 948	D	--
IM000615	CATGTCTACTTTATTGCATATTAGGA TGTCAGGTCCTGCTCGTTTCCTGGG ACCATTTGCCTGGAAGACATTTTCC ATTCTTTTACTCTGAGATAGTTCCTG TCTTTGTTGTTGAGGTGTGTTTCTTG TATTCAGCAAAATGCTGGATCTTGTT TGCGAATCCAGTCTGTTAGCTTATGT CTTTTACAGGTGAATTGAGTCCATT AATATTGAGAGATATTAAGAGAAAT GACTTTTGGTTCCTGATATATTTGTTT TTCTAGTTAGTTTGTGTGCTTGGA	469 949	D	--

	CTCTCTCCCTTTGACTGTGTTGTGAG ATGCTTAATATCTTGTCTATCTTTG GTGCAGGTGTCTTCCTTGTGTTAGA GTTTTCAATCCAGGTTTCTCTGTAGT GTTATGTTAGAAGACATATACTGCTT GAATTTAGTTTTGCCTGGAATATTTT GTTTTCTCCATCTATGTTGATTGAGA GTTTTCTGGGTAAAATAGCCTANCC TGGCATTTGTGTTCTCTTAAAAGTCT GTATGACCTCTGACTANGCTTTTCTG GCC			
IM000616	CATGGTGAATGATTGTTTTGATGTGT TCTTGGATTGGTTTCGAGAATTTTA TTGACTATTTTGGCATTAACTCATA AGGGAAATTGGTCTGAAGTTCTTCC TTGTTGAGTCTTTATGAGGGTATCAA TATAATTGTGGATTCATAGAGCAAGT TGGATTGTGTTCTTCTGTTTATATTT TGTGGAATATTTGAAGAGTATTGGT ATTAGATTTTCTTGAAGGTATGATA GAATTCTGAACTAAACCCATATGGTT CTGGATTTTTTTGGTTGGAAGACCA ATGACTGCTTCTATTTCTTTAGGTGT TATGGGACTGTATAGATGGTTTATCT GAACCAGATTTAACTTTGGTATTTGT TATCTGTTTAGAAAATTGCCCATTTT ATCCATATTTCCAGTTGTGTTGAGT ATAGGCTTTTGTAGTAGGATATAATG ATTTTTGAATTTCTCAGTATGTTTT CTTATATCTCCCTTTCCATTTCTGATT TTGTTAATGTGGATACTATCTCCGTG TCCCC	470 950	R	--
IM000617	CCATGTCAGGTGGTTAACCTGTGAGTCTAAC TTCCAGGAATGCAATGCCTCTGGCATCTACA GGCATAAACATACTTGTGGCTTACACTCAAAC TGACACACCAACACATATGTGCACGCGCACA CACACACACACCAAATTAATAATAAATAACC CTTTTTAAAAAATATAGAATCTATAGATAATT GCTTTACTGCACTCACAACATTTTAGGATC	474 951	D	--
IM000618	ACACTAACACAAAGAAGGGGATC	472 952	D	--